GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:13 ; Search time 9258.62 Seconds
(without alignments)
3097.698 Million cell updates/sec

Title: US-09-827-854A-2
Perfect score: 1493
Sequence: 1 KVEQAVETEPEPELRQQTEW.....VEKVQAAVGTSAAPVPSDNH 299

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1493	100.0	1110	2	E00359	E00359 cDNA coding
2	1493	100.0	1110	2	E00823	E00823 DNA sequenc
3	1493	100.0	1147	2	AX302545	AX302545 Sequence
4	1493	100.0	1156	2	BD004278	BD004278 Apo E hum
5	1493	100.0	1156	2	CQ785970	CQ785970 Sequence
6	1493	100.0	1156	2	CQ875269	CQ875269 Sequence
7	1493	100.0	1156	2	CQ896276	CQ896276 Sequence
8	1493	100.0	1156	2	CQ963896	CQ963896 Sequence
9	1493	100.0	1156	2	CQ981476	CQ981476 Sequence
10	1493	100.0	1156	2	DD166083	DD166083 Treatment
11	1493	100.0	1156	2	AR380462	AR380462 Sequence
12	1493	100.0	1156	2	AX821568	AX821568 Sequence
13	1493	100.0	1156	5	HUMAPOE3	K00396 Homo sapien
14	1493	100.0	1186	5	BC003557	BC003557 Homo sapi
15	1493	100.0	1291	2	AR531680	AR531680 Sequence
16	1493	100.0	1550	5	BC072022	BC072022 Homo sapi
17	1486	99.5	1110	2	E08423	E08423 DNA coding
18	1485	99.5	1156	2	BD004277	BD004277 Apo E hum
19	1484	99.4	1157	2	DD166085	DD166085 Treatment
20	1484	99.4	1157	2	I15975	I15975 Sequence 1
21	1484	99.4	1157	2	AX333278	AX333278 Sequence
22	1484	99.4	1157	2	AX409597	AX409597 Sequence
23	1484	99.4	1157	5	HUMAPOE	M12529 Human apoli
24	1481	99.2	900	2	BD064748	BD064748 Method fo
25	1481	99.2	1156	2	BD004279	BD004279 Apo E hum
26	1481	99.2	1156	2	CQ719877	CQ719877 Sequence
27	1370.5	91.8	1107	2	BD084811	BD084811 Diagnosis
28	1369.5	91.7	5491	5	AF261279	AF261279 Homo sapi
29	1369.5	91.7	41907	2	AX358722	AX358722 Sequence
30	1369.5	91.7	41907	5	AF050154	AF050154 Homo sapi
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32	1363.5	91.3	3805	2	BD231977	BD231977 Methods a
33	1363.5	91.3	3805	2	AR282772	AR282772 Sequence
34	1359	91.0	1178	5	MFAPOE	X13887 Monkey mRNA
35	1351.5	90.5	5515	2	DD166084	DD166084 Treatment
36	1351.5	90.5	5515	5	HUMAPOE4	M10065 Human apoli
37	1323	88.6	5413	5	AF261280	AF261280 Pan trogl
38	1315	88.1	39483	12	AC146473	AC146473 Hylobates
39	1270.5	85.1	183798	12	AC145523	AC145523 Papio ham
40	1254.5	84.0	191327	12	AC151887	AC151887 Saimiri b
41	1240	83.1	4762	5	BABAPOE	M29322 Baboon apol
c 42	1239	83.0	208239	12	AC021988	AC021988 Homo sapi
43	1205	80.7	1138	14	AF303830	AF303830 Tupaia gl
44	1151	77.1	718	5	AF200497S3	AF200499 Pan trogl
45	1147	76.8	718	5	AF200500S3	AF200502 Gorilla g

ALIGNMENTS

RESULT 1
E00359
LOCUS E00359 1110 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA coding human apolipoprotein E3.
ACCESSION E00359
VERSION E00359.1 GI:2168646
KEYWORDS JP 1985118189-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Teranishi,Y., Takamatsu,N., Matsui,Y., Kimura,M. and Ikeda,Y.
TITLE DNA FRAGMENT
JOURNAL Patent: JP 1985118189-A 1 25-JUN-1985;
MITSUBISHI CHEM IND LTD
COMMENT OS human
PN JP 1985118189-A/1
PD 25-JUN-1985
PF 29-NOV-1983 JP 1983224980
PI TERANISHI YUTAKA, TAKAMATSU NOBUHIKO, MATSUI YASUSHI, PI
KIMURA MASAKO,
PI IKEDA YASUKO
PC C12N15/00,C07H21/04//C12P21/00;
CC strandedness: Double;
CC topology: Linear;

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            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: tissue_type=liver;
            FH   Key             Location/Qualifiers
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            sig_peptide     15. .68
            FT                   /product='apolipoprotein E3 signal peptide' FT
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FEATURES             Location/Qualifiers
     source          1. .1110
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
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ORIGIN

Alignment Scores:
Pred. No.:              1.04e-120       Length:         1110
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x E00359 (1-1110)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        129 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 188

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        189 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 248

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        369 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 428

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        429 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 488

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        489 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 548

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        609 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 668

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        669 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 728

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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RESULT 2
E00823
LOCUS       E00823                  1110 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence coding for human apolipoprotein E and its signal
            peptide.
ACCESSION   E00823
VERSION     E00823.1  GI:2169084
KEYWORDS    JP 1986096997-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Teranishi,Y., Matsui,Y., Ikeda,Y. and Kimura,M.
  TITLE     PRODUCTION OF HUMAN APOLIPOPROTEIN E-LIKE PROTEIN
  JOURNAL   Patent: JP 1986096997-A 1 15-MAY-1986;
            MITSUBISHI CHEM IND LTD
COMMENT     OS   Human {Homo sapiens}
            PN   JP 1986096997-A/1
            PD   15-MAY-1986
            PF   16-OCT-1984 JP 1984216987
            PI   TERANISHI YUTAKA, MATSUI YASUSHI, IKEDA YASUKO, KIMURA MASAKO
            PC   C12P21/00,A61K35/74,A61K37/04,C12N15/00,(C12P21/00,C12R1:19),
            PC   (C12N15/00,
            PC   C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: tissue_type=Liver;
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ORIGIN

Alignment Scores:
Pred. No.:              1.04e-120       Length:         1110
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x E00823 (1-1110)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db         129 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 188

Qy          41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db         189 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 248

Qy          61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db         249 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 308

Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db         309 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 368

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Qy         181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Qy         221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Qy         241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db         789 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 848

Qy         261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db         849 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 908

Qy         281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Db         909 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 965

RESULT 3
AX302545
LOCUS       AX302545               1147 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 63 from Patent WO0175177.
ACCESSION   AX302545
VERSION     AX302545.1  GI:17383082
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
  TITLE     Tumor markers in ovarian cancer
  JOURNAL   Patent: WO 0175177-A 63 11-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .1147
                     /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.:                1.08e-120      Length:          1147
Score:                    1493.00        Matches:         299
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-09-827-854A-2 (1-299) x AX302545 (1-1147)

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Qy          21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db         160 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 219

Qy          41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Qy         101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Qy         121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Qy         201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db         700 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 759

Qy         221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 819

Qy         241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 879

Qy         261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         880 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 939
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Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 996

RESULT 4
BD004278
LOCUS       BD004278                1156 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Apo E humanized mammal.
ACCESSION   BD004278
VERSION     BD004278.1  GI:18632239
KEYWORDS    JP 2001017028-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1156)
  AUTHORS   Fujita,S., Hamanaka,H., Fukui,Y. and Yokoyama,M.
  TITLE     Apo E humanized mammal
  JOURNAL   Patent: JP 2001017028-A 2 23-JAN-2001;
            MITSUBISHI CHEMICAL CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001017028-A/2
            PD   23-JAN-2001
            PF   28-APR-2000 JP 2000128919
            PR
            PI   SHINOBU FUJITA,HIROKI HAMANAKA,YUKO FUKUI,MINESUKE YOKOYAMA PC
              A01K67/027,A61K45/00,A61P25/28,A61P43/00,C12N5/10, PC
            C12N15/09//C07K14/775,
            PC   (C12N5/10,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91) CC

            FH   Key             Location/Qualifiers
            FT   CDS             (61). .(1011).
FEATURES              Location/Qualifiers
     source           1. .1156
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x BD004278 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 5
CQ785970
LOCUS       CQ785970                1156 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 11 from Patent EP1398032.
ACCESSION   CQ785970
VERSION     CQ785970.1  GI:45721147
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kober,I., Albers,M., Koegl,M., Blume,B., Deuschle,U. and
            Kremoser,C.
  TITLE     4-Oxo-quinazolines as LXR nuclear receptor binding compounds
  JOURNAL   Patent: EP 1398032-A 11 17-MAR-2004;
            PheneX Pharmaceuticals AG (DE)
FEATURES              Location/Qualifiers
     source           1. .1156
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x CQ785970 (1-1156)
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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 6
CQ875269
LOCUS       CQ875269                1156 bp    DNA     linear   PAT 27-SEP-2004
DEFINITION  Sequence 12 from Patent WO2004076613.
ACCESSION   CQ875269
VERSION     CQ875269.1  GI:52748357
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Herr,A., Hinzmann,B., Dahl,E., Staub,E., Pilarsky,C. and Specht,T.
  TITLE     Human nucleic acid sequences from carcinomas of the bladder
  JOURNAL   Patent: WO 2004076613-A 12 10-SEP-2004;
            Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE);
            Staub, Eike (DE); Pilarsky, Christian (DE); Specht, Thomas (DE)
FEATURES             Location/Qualifiers
     source          1. .1156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.09e-120      Length:          1156
Score:                    1493.00        Matches:         299
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-09-827-854A-2 (1-299) x CQ875269 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894
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Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 7
CQ896276
LOCUS       CQ896276               1156 bp    DNA     linear   PAT 05-NOV-2004
DEFINITION  Sequence 100 from Patent WO2004076614.
ACCESSION   CQ896276
VERSION     CQ896276.1  GI:55468125
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hinzmann,B., Dahl,E., Rosenthal,A., Specht,T., Schmitt,A.,
            Beckmann,G., Bruemmendorf,T., Kinnemann,H., Roepcke,S., Hermann,K.,
            Xinzhong,L., Pilarsky,C. and Staub,E.
  TITLE     Human nucleic acid sequences obtained from prostatic carcinomas
  JOURNAL   Patent: WO 2004076614-A 100 10-SEP-2004;
            Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);
            Specht, Thomas (DE); Schmitt, Armin (DE)
FEATURES             Location/Qualifiers
     source          1. .1156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x CQ896276 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 8
CQ963896
LOCUS       CQ963896               1156 bp    DNA     linear   PAT 13-DEC-2004
DEFINITION  Sequence 19 from Patent WO2004104224.
ACCESSION   CQ963896
VERSION     CQ963896.1  GI:56562665
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wright,M.B.
  TITLE     Markers for lxr activation
  JOURNAL   Patent: WO 2004104224-A 19 02-DEC-2004;
            F. Hoffmann-La Roche AG (CH)
FEATURES             Location/Qualifiers
     source          1. .1156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x CQ963896 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60

Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80

Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100

Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160

Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220

Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240

Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260

Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280

Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299

Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 9
CQ981476
LOCUS       CQ981476               1156 bp    DNA     linear   PAT 25-JAN-2005
DEFINITION  Sequence 331 from Patent EP1498424.
ACCESSION   CQ981476
VERSION     CQ981476.1  GI:58190766
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosenthal,A., Hermann,K., Heiden,E., Pilarsky,C., Bruemmendorf,T.,
            Staub,E., Roepcke,S., Mennerich,D., Kinnemann,H. and Li,X.
  TITLE     Human nucleic acid sequences from lung tumours
  JOURNAL   Patent: EP 1498424-A 331 19-JAN-2005;
            Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);
            Rosenthal, Andre (DE)
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FEATURES             Location/Qualifiers
     source          1. .1156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.09e-120      Length:          1156
Score:                    1493.00        Matches:         299
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       2              Gaps:            0

US-09-827-854A-2 (1-299) x CQ981476 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20

Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40

Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60

Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80

Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100

Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160

Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220

Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240

Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260

Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280

Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954
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Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 10
DD166083
LOCUS       DD166083                1156 bp    DNA     linear   PAT 23-NOV-2005
DEFINITION  Treatments for Age Related-Macular Degeneration.
ACCESSION   DD166083
VERSION     DD166083.1  GI:83962539
KEYWORDS    JP 2005511713-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1156)
  AUTHORS   Ishida,B., Kern,J., Duncan,K., Bailey,C. and Schwartz,D.M.
  TITLE     Treatments for Age Related-Macular Degeneration
  JOURNAL   Patent: JP 2005511713-A 1 28-APR-2005;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Human
            PN   JP 2005511713-A/1
            PD   28-APR-2005
            PF   06-DEC-2002 JP 2003550736
            PR   03-OCT-2002 US    60/415864,07-DEC-2001 US    60/340498 PI
            brian ishida,john kern,keith duncan,cathy bailey,daniel m  PI
            schwartz
            CC
            FH   Key             Location/Qualifiers
FEATURES              Location/Qualifiers
     source           1. .1156
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x DD166083 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 11
AR380462
LOCUS       AR380462                1156 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1007 from patent US 6607879.
ACCESSION   AR380462
VERSION     AR380462.1  GI:40088096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1156)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1007 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES              Location/Qualifiers
     source           1. .1156
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x AR380462 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234
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Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 12
AX821568
LOCUS       AX821568                1156 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 1 from Patent WO03068986.
ACCESSION   AX821568
VERSION     AX821568.1  GI:39724945
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turcatti,G.
  TITLE     Nucleotide detection by fluorescence resonance energy transfer and
            methods thereof
  JOURNAL   Patent: WO 03068986-A 1 21-AUG-2003;
            Applied Research Systems ARS Holding N.V. (AN)
FEATURES             Location/Qualifiers
     source          1. .1156
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-120       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x AX821568 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 13
HUMAPOE3
LOCUS       HUMAPOE3                1156 bp    mRNA    linear   PRI 21-OCT-2002
DEFINITION  Homo sapiens preapolipoprotein E (APOE) mRNA, complete cds.
ACCESSION   K00396
VERSION     K00396.1  GI:178850
KEYWORDS    apolipoprotein; apolipoprotein E; lipoprotein; polymorphism; very
            low density lipoprotein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 355 to 1156)
  AUTHORS   Breslow,J.L., McPherson,J., Nussbaum,A.L., Williams,H.W.,
            Lofquist-Kahl,F., Karathanasis,S.K. and Zannis,V.I.
  TITLE     Identification and DNA sequence of a human apolipoprotein E cDNA
            clone
  JOURNAL   J. Biol. Chem. 257 (24), 14639-14641 (1982)
   PUBMED   6897404
REFERENCE   2  (bases 250 to 777)
  AUTHORS   Wallis,S.C., Rogne,S., Gill,L., Markham,A., Edge,M., Woods,D.,
            Williamson,R. and Humphries,S.
  TITLE     The isolation of cDNA clones for human apolipoprotein E and the
            detection of apoE RNA in hepatic and extra-hepatic tissues
  JOURNAL   EMBO J. 2 (12), 2369-2373 (1983)
   PUBMED   6199196
REFERENCE   3  (bases 1 to 1156)
  AUTHORS   Zannis,V.I., McPherson,J., Goldberger,G., Karathanasis,S.K. and
            Breslow,J.L.
  TITLE     Synthesis, intracellular processing, and signal peptide of human
            apolipoprotein E
  JOURNAL   J. Biol. Chem. 259 (9), 5495-5499 (1984)
   PUBMED   6325438
REFERENCE   4  (bases 88 to 1156)
  AUTHORS   McLean,J.W., Elshourbagy,N.A., Chang,D.J., Mahley,R.W. and
            Taylor,J.M.
  TITLE     Human apolipoprotein E mRNA. cDNA cloning and nucleotide sequencing
            of a new variant
  JOURNAL   J. Biol. Chem. 259 (10), 6498-6504 (1984)
   PUBMED   6327682
REFERENCE   5  (bases 577 to 624)
  AUTHORS   Gill,L.L., Peoples,O.P., Pearston,D.H., Robertson,F.W.,
            Humphries,S.E., Cumming,A.M. and Hardman,N.
  TITLE     Isolation and characterisation of a variant allele of the gene for
            human apolipoprotein E
  JOURNAL   Biochem. Biophys. Res. Commun. 130 (3), 1261-1266 (1985)
   PUBMED   2992507
REFERENCE   6  (sites)
  AUTHORS   Rall,S.C. Jr., Newhouse,Y.M., Clarke,H.R., Weisgraber,K.H.,
            McCarthy,B.J., Mahley,R.W. and Bersot,T.P.
  TITLE     Type III hyperlipoproteinemia associated with apolipoprotein E
            phenotype E3/3. Structure and genetics of an apolipoprotein E3
            variant
  JOURNAL   J. Clin. Invest. 83 (4), 1095-1101 (1989)
   PUBMED   2539388
COMMENT     [1]  corrected in [J. Biol. Chem. 258, 11422-11422 (1983)]. [J.
            Biol. Chem. 258, 11422-11422 (1983)]  correction of [1]. [4]
            epsilon-3 and variant.
            [5]  epsilon-2 allele.
            [6]  sites; mutations resulting in type III hyperlipoproteinemia.
            Apo E is a component of normal human very low density lipoprotein.
            There are six human apo E phenotypes known to result from a single
            structural gene, three of the common alleles being epsilon-4,
            epsilon-3 and epsilon-2. This sequence appears to be of the
            epsilon-3 allele. [1] argues that the apo E polymorphism involves
            mutations in the structural coding region; for example the
            epsilon-2 phenotype which is characterized by hyperlipoproteinemia
            is thought to result from a c to t change (arg to cys) at base 586
            below [3],[5]. The sequence shown is 57% homologous with human apo
            A-I and 81% homologous with rat apo E. For the epsilon-4 sequence,
            see the separate entry.
            [J. Biol. Chem. 258, 11422-11422 (1983)] is too extensively revised
            relative to [1] to record the
            revisions in the FEATURES table. The sequence below is that of [J.
            Biol. Chem. 258, 11422-11422 (1983)]
            and [3].
            Apo E  is located on chromosome 19 --Jackson, Bruns and Breslow ,
            PNAS USA 81, 2945-2949 (1984) -- and is believed to be linked to
            the Apo C-II gene (see separate entry).
            The two mutations causing type III hyperlipoproteinemia
            (apolipoprotein E phenotype E3/3) produces substitutions of Arg for
            Cys at amino acid 112 and Cys for Arg at amino acid position 142.
            Draft entry and printed copy of sequence for [1] kindly provided by
            L.L. Gill, University of Aberdeen.
            Complete source information:
            Human liver [1],[J. Biol. Chem. 258, 11422-11422 (1983)],[2],[3],
            [4] and blood [5], cDNA to mRNA.
FEATURES             Location/Qualifiers
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                     /map="19q13.2"
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                     KLRKRLLRDADDLQKRLAVYQAGAREGAERGLSAIRERLGPLVEQGRVRAATVGSLAG
                     QPLQERAQAWGERLRARMEEMGSRTRDRLDEVKEQVAEVRAKLEEQAQQIRLQAEAFQ
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ORIGIN

Alignment Scores:
Pred. No.:                1.09e-120      Length:          1156
Score:                    1493.00        Matches:         299
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       5              Gaps:            0

US-09-827-854A-2 (1-299) x HUMAPOE3 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 14
BC003557
LOCUS       BC003557                1186 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens apolipoprotein E, mRNA (cDNA clone MGC:1571
            IMAGE:3355712), complete cds.
ACCESSION   BC003557
VERSION     BC003557.1  GI:13097698
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1186)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
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REFERENCE   2  (bases 1 to 1186)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 6 Row: h Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4557324.
FEATURES             Location/Qualifiers
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                     /note="synonym: MGC1571"
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ORIGIN

Alignment Scores:
Pred. No.:                1.13e-120       Length:          1186
Score:                    1493.00         Matches:         299
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       5               Gaps:            0

US-09-827-854A-2 (1-299) x BC003557 (1-1186)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        160 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 219

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        460 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 519

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        520 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 579

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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RESULT 15
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LOCUS       AR531680                1291 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 246 from patent US 6727066.
ACCESSION   AR531680
VERSION     AR531680.1  GI:53920119
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1291)
  AUTHORS   Kaser,M.R.
  TITLE     Genes expressed in treated human C3A liver cell cultures
  JOURNAL   Patent: US 6727066-A 246 27-APR-2004;
            Incyte Corporation; Palo Alto, CA
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FEATURES             Location/Qualifiers
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Alignment Scores:
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Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x AR531680 (1-1291)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299

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Search completed: June 14, 2006, 21:46:14
Job time : 9268.62 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 18:51:12 ; Search time 1029.05 Seconds
(without alignments)
3038.776 Million cell updates/sec

Title: US-09-827-854A-2
Perfect score: 1493
Sequence: 1 KVEQAVETEPEPELRQQTEW.....VEKVQAAVGTSAAPVPSDNH 299

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	1493	100.0	1147	5	ABA83113	Aba83113 Apolipopr
5	1493	100.0	1154	13	ADQ86961	Adq86961 Human tum
6	1493	100.0	1156	4	AAF84315	Aaf84315 Human Apo
7	1493	100.0	1156	6	ABT13008	Abt13008 Human apo
8	1493	100.0	1156	6	AAD22048	Aad22048 Human apo
9	1493	100.0	1156	8	ACA64743	Aca64743 Apolipopr
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33	1493	100.0	1291	8	ABX63454	Abx63454 Human cDN
34	1493	100.0	1291	9	ACH04051	Ach04051 Human cDN
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ALIGNMENTS

RESULT 1
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ID AAD26035 standard; cDNA; 954 BP.
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AC AAD26035;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human apolipoprotein E (APOE) cDNA.
XX
KW Human; antilipaemic; neuroprotective; nootropic; genetic variant; APOE;
KW apolipoprotein E; haplotyping; familial dysbetalipoproteinaemia; therapy;
KW genotyping; type III hyperlipoproteinaemia; Alzheimer's disease; SNP;
KW atherosclerosis; single nucleotide polymorphism; chromosome 19q13.2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PF   16-APR-2001; 2001WO-US012303.
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PR   14-APR-2000; 2000US-0197188P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kliem SE,  Koshy B,  Lee HH;
XX
DR   WPI; 2002-075064/10.
DR   P-PSDB; AAE15158.
XX
PT   Genotyping human apolipoprotein gene of individual for determining
PT   haplotype of individual, involves determining identity of nucleotide pair
PT   at specific polymorphic sites for two copies of gene.
XX
PS   Claim 26; Fig 2; 78pp; English.
XX
CC   The patent discloses novel genetic variants of human apolipoprotein E
CC   (APOE) gene. The invention also relates to compositions and methods for
CC   haplotyping and/or genotyping the APOE gene. The haplotyping methods of
CC   the invention are useful for improving the efficacy and reliability of
CC   several steps in the discovery and development of drugs for treating
CC   diseases associated with APOE activity, e.g. familial
CC   dysbetalipoproteinaemia, type III hyperlipoproteinaemia, atherosclerosis,
CC   and Alzheimer's disease. They are useful to validate APOE as a candidate
CC   agent for treating a specific condition or disease predicted to be
CC   associated with APOE activity and in the design of clinical trials of
CC   candidate drugs for treating a specific condition or disease predicted to
CC   be associated with APOE activity. Genotyping or haplotyping methods are
CC   useful to screen for compounds targeting APOE to treat a specific
CC   condition or disease associated with APOE activity. The present sequence
CC   is a cDNA encoding human APOE protein. APOE gene is located on chromosome
CC   19q13.2
XX
SQ   Sequence 954 BP; 168 A; 290 C; 377 G; 119 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              9.13e-107      Length:         954
Score:                  1493.00        Matches:        299
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-09-827-854A-2 (1-299) x AAD26035 (1-954)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        835 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 894

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 951

RESULT 2
ADV42852
ID   ADV42852 standard; cDNA; 954 BP.
XX
AC   ADV42852;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 480.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004108899-A2.
XX
PD   16-DEC-2004.
XX
```

PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 480; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 954 BP; 168 A; 290 C; 377 G; 119 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.13e-107	Length:	954
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-09-827-854A-2 (1-299) x ADV42852 (1-954)

```
Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 114

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 174

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 234

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 294

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 354

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 414

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 474

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 534

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 594

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 654

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 714

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 774

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 834

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 894

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 951
```

RESULT 3
AAN60409
ID AAN60409 standard; DNA; 1110 BP.
XX
AC AAN60409;
XX
DT 25-MAR-2003 (revised)
DT 01-JAN-1980 (first entry)
XX
DE Human apolipoprotein-E.
XX
KW Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 15. .968
FT /*tag= a
XX
PN AU8547513-A.
XX
PD 24-APR-1986.
XX
PF 17-SEP-1985; 85AU-00047513.
XX
PR 16-OCT-1984; 84JP-00216987.
PR 11-JUN-1985; 85JP-00126989.
XX
PA (MITU) MITSUBISHI CHEM IND LTD.
XX
DR WPI; 1986-150217/24.
DR P-PSDB; AAP60507.
XX
PT New DNA sequence coding for human apolipoprotein-E - and expression
PT vectors and transformed cells contg. it.
XX
PS Disclosure; Fig 2; 45pp; English.
XX
CC The encoded protein is used to treat subjects who are deficient in
CC apolipoprotein-E (or who produce abnormal forms of this molecule) and
CC therefore are likely to suffer from hyperlipidemia, resulting in
CC arteriosclerosis. It can also be used to raise antisera for detecting the
CC protein deficiency or production of abnormal forms. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1110 BP; 198 A; 354 C; 415 G; 143 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.08e-106	Length:	1110
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-09-827-854A-2 (1-299) x AAN60409 (1-1110)

```
Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 128

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 188

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 248

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 308

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 368

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CAGGCCCGGCTGGGCGCCGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 428

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 488

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 548

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 608

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 668

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 728

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 788

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 848

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 908

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 965
```

RESULT 4
ABA83113
ID ABA83113 standard; DNA; 1147 BP.
XX
AC ABA83113;
XX
DT 08-FEB-2002 (first entry)
XX
DE Apolipoprotein E ovarian tumour marker gene, SEQ ID NO:63.
XX
KW Ovarian tumour marker gene; human; overexpression; upregulation;
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localised; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200175177-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010947.
XX
PR 03-APR-2000; 2000US-0194336P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
XX
DR WPI; 2001-626450/72.
DR P-PSDB; ABB50287.
XX
PT Detecting and identifying ovarian tumor, identifying increased risk for
PT developing ovarian cancer, and determining effectiveness of ovarian
PT cancer treatment, by measuring expression level of ovarian tumor marker
PT gene.
XX
PS Claim 23; Page 105-106; 140pp; English.
XX
CC The invention relates to methods for diagnosing and prognosing ovarian
CC tumours in an individual via the detection and measurement of the
CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
CC ABA83181 and ABA83183). The methods of the invention are useful for
CC detecting an ovarian tumour in a patient, for identifying an individual
CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
CC mucinous cystadenoma, borderline mucinous tumour, mucinous
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes or their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184 represent the ovarian tumour marker genes of the
CC invention
XX
SQ Sequence 1147 BP; 210 A; 365 C; 425 G; 147 T; 0 U; 0 Other;

Alignment Scores:

```
Pred. No.:              1.12e-106       Length:         1147
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     5               Gaps:           0

US-09-827-854A-2 (1-299) x ABA83113 (1-1147)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 159

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 219

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 279

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 339

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 399

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 459

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 519

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 579

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 639

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 699

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 759

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 819

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 879

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 939

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 996

RESULT 5
ADQ86961
ID   ADQ86961 standard; cDNA; 1154 BP.
XX
AC   ADQ86961;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #3836.
XX
KW   human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW   cancer; cell proliferative disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004060270-A2.
XX
PD   22-JUL-2004.
XX
PF   15-OCT-2003; 2003WO-US029126.
XX
PR   18-OCT-2002; 2002US-0418988P.
XX
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
XX
PI   Wu TD,  Zhou Y;
XX
DR   WPI; 2004-534300/51.
XX
PT   New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer.
XX
PS   Claim 1; SEQ ID NO 3836; 5504pp; English.
XX
CC   The present invention describes an isolated tumour-associated antigenic
CC   target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC   sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC   (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC   sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC   (c). Also described: (1) an expression vector comprising the above
CC   nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC   a process for producing a polypeptide; (4) an isolated polypeptide
CC   comprising: (a) an amino acid sequence encoded by any of the above
CC   nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC   length coding region of the above nucleotide sequences; or (c) a sequence
CC   having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC   comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC   an isolated antibody that binds to the above polypeptide; (7) a process
CC   for producing the antibody; (8) an isolated oligopeptide that binds to
CC   the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC   binding organic molecule that binds to the above polypeptide; (10) a
CC   composition of matter comprising the above (chimeric) polypeptide,
CC   antibody, oligopeptide or TAT binding organic molecule, in combination
CC   with a carrier; (11) an article of manufacture comprising a container and
CC   the composition of matter contained within the container; (12) methods of
CC   inhibiting the growth of a cell that expresses the above protein, where
CC   the growth of the cell is at least in part dependent upon a growth
CC   potentiating effect of the above protein; (13) a method of
CC   therapeutically treating a mammal having a cancerous tumour comprising
CC   cells that express the above protein; (14) a method of determining the
CC   presence of a protein in a sample suspected of containing the protein
CC   described above; (15) methods of diagnosing the presence of a tumour in a
CC   mammal; (16) a method for treating or preventing a cell proliferative
CC   disorder associated with increased expression or activity of the above
CC   protein; and (17) a method of binding an antibody, oligopeptide or
CC   organic molecule to a cell that expresses the protein described above.
CC   The TAT sequences have cytostatic activities, and can be used in gene
CC   therapy. The composition and methods are useful for diagnosing,
CC   preventing or treating cancer. The composition is also used for preparing
CC   a medicament for the therapeutic treatment or diagnostic detection of a
CC   cell proliferative disorder or cancer. The present sequence represents a
CC   human TAT cDNA sequence from the present invention.
XX
SQ   Sequence 1154 BP; 208 A; 367 C; 431 G; 148 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              1.13e-106      Length:          1154
Score:                  1493.00        Matches:         299
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     13             Gaps:            0

US-09-827-854A-2 (1-299) x ADQ86961 (1-1154)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 172

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 232

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 292

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 352

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 412

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 472

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 532

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 592

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 652

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 712

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 772

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 832

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 892

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 952

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1009

RESULT 6
AAF84315
ID   AAF84315 standard; cDNA; 1156 BP.
XX
AC   AAF84315;
XX
DT   21-JUN-2001  (first entry)
XX
DE   Human ApoE3 coding sequence.
XX
KW   Human; ApoE3; Alzheimer's disease; arteriosclerosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             61. .1014
FT                   /*tag=  a
FT                   /product= "Human ApoE3"
XX
PN   JP2001017028-A.
XX
PD   23-JAN-2001.
XX
PF   28-APR-2000; 2000JP-00128919.
XX
PR   06-MAY-1999;   99JP-00125647.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
DR   WPI; 2001-285406/30.
DR   P-PSDB; AAB80997.
XX
PT   New apoE humanized mammalian cell useful for screening for agents useful
PT   for treating or preventing Alzheimer's disease and arteriosclerosis.
XX
PS   Disclosure; Page 13-14; 22pp; Japanese.
XX
CC   The present invention relates to an ApoE humanised mammalian cell. The
CC   present sequence is the coding sequence for human ApoE3, which was used
CC   in the method of the present invention. The ApoE humanised mammalian cell
CC   can be used for screening for agents useful for treating or preventing
CC   Alzheimer's disease and arteriosclerosis
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-106      Length:          1156
Score:                  1493.00        Matches:         299
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     4              Gaps:            0

US-09-827-854A-2 (1-299) x AAF84315 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
```

RESULT 7
ABT13008
ID ABT13008 standard; DNA; 1156 BP.
XX
AC ABT13008;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human apolipoprotein E (APOE) gene.
XX
KW Human; gene; ds; gene therapy; single nucleotide polymorphism; SNP;
KW cytochrome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1;
KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW glycosylphosphatidylinositol-1; low serum high density lipoprotein.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT variation   replace(197, C)
FT   /*tag= a
FT   /note= "Single nucleotide polymorphism"
FT variation   replace(448, C)
FT   /*tag= b
FT   /note= "Single nucleotide polymorphism"
FT variation   replace(540, T)
FT   /*tag= c
FT   /note= "Single nucleotide polymorphism"
FT variation   replace(586, T)
FT   /*tag= d
FT   /note= "Single nucleotide polymorphism"
XX
PN WO200272604-A2.
XX
PD 19-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US006728.
XX
PR 09-MAR-2001; 2001US-00802640.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Braun A, Bansal A, Kleyn PW;
XX
DR WPI; 2002-750478/81.
DR P-PSDB; AAO15886.
XX
PT Detecting the presence or absence of an allelic variant of a polymorphic
PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
PT to high serum cholesterol, low serum HDL and cardiovascular disease.
XX
PS Disclosure; Page 118-119; 199pp; English.
XX
CC The invention comprises methods of detecting the presence or absence of
CC at least one allelic variant of a polymorphic region of a gene associated
CC with cardiovascular disease. The invention specifically relates to
CC detecting the region of a cytochrome C oxidase subunit VIb (COX6B) gene
CC that is associated with high serum cholesterol, or the region of the N-
CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
CC (GPI-1) gene that is associated with low serum high density lipoprotein
CC (HDL). The methods of the invention are useful for detecting a
CC predisposition to high serum cholesterol, low serum HDL and
CC cardiovascular disease. The methods are also useful for elucidating
CC pathological pathways, developing diagnostic assays and new drug
CC therapies for such disorders. The present DNA sequence represents a human
CC gene associated with high serum cholesterol, low serum HDL and/or
CC cardiovascular disease
XX
SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-106	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-2 (1-299) x ABT13008 (1-1156)

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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534
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Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
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RESULT 8
AAD22048
ID AAD22048 standard; DNA; 1156 BP.
XX
AC AAD22048;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human apolipoprotein E (apoE) isoprotein, apoE3 DNA.
XX
KW Human; apolipoprotein E; apoE; cholesterol; atherosclerosis;
KW hypertriglyceridaemia; low density lipoprotein; LDL; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61. .1014
FT /*tag= a
FT /product= "Human apoE isoprotein, apoE3"
FT sig_peptide 61. .114
FT /*tag= b
FT mat_peptide 115. .1011
FT /*tag= c
FT /product= "Mature human apoE isoprotein, apoE3"
XX
PN WO200177136-A1.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011358.
XX
PR 06-APR-2000; 2000US-00544386.
PR 04-OCT-2000; 2000US-00679088.
PR 05-APR-2001; 2001US-00827854.
XX
PA (KOSP-) KOS PHARM INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Zannis VI, Kypreos KE;
XX
DR WPI; 2002-010885/01.
DR P-PSDB; AAE13294.
XX
PT New apolipoprotein E polypeptide and nucleic acid, useful for lowering
PT cholesterol, delaying the onset of or treating atherosclerosis in mammal,
PT without inducing hypertriglyceridemia.
XX
PS Claim 14; Page 81; 91pp; English.
XX
CC The present sequence is a human apolipoprotein E (apoE) isoprotein, apoE3
CC DNA. The apoE lipoproteins are useful for lowering cholesterol, delaying
CC the onset of atherosclerosis, treating or regressing atherosclerosis
CC without inducing hypertriglyceridaemia, in a mammal lacking an
CC endogenous, normally functioning apoE gene or low density lipoprotein
CC (LDL) receptor or is at risk for developing atherosclerosis due to
CC accumulation of lipoprotein remnants in the bloodstream or having a
CC defect in remnant removal
XX
SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-106	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-2 (1-299) x AAD22048 (1-1156)

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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774
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```
Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 9
ACA64743
ID   ACA64743 standard; DNA; 1156 BP.
XX
AC   ACA64743;
XX
DT   18-JUN-2003  (first entry)
XX
DE   Apolipoprotein gene #3.
XX
KW   Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;
KW   apoptosis; gene therapy; mammalian cell receptor; cytostatic;
KW   tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW   tumouricidal immunocyte; antitumour.
XX
OS   Unidentified.
XX
PN   US2002177551-A1.
XX
PD   28-NOV-2002.
XX
PF   30-MAY-2001; 2001US-00870759.
XX
PR   31-MAY-2000; 2000US-0208128P.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2003-361759/34.
DR   P-PSDB; ABU79141.
XX
PT   A mammalian cell receptor, useful in the treatment of cancer by binding
PT   to tumor associated lipids where the binding induces anergy or apoptosis
PT   in T cells and antigen presenting cells.
XX
PS   Example 2; Page; 167pp; English.
XX
CC   The invention relates to a mammalian cell receptor, useful in the
CC   treatment of cancer, which binds to tumour associated lipids and induces
CC   anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC   Also included are a mammalian cell useful in the treatment of cancer
CC   where the receptor which binds tumour associated lipids and induces
CC   cellular inactivation or death is deleted or functionally deactivated,
CC   producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC   (by allowing tumour associated lipids to contact immunocytes in which
CC   receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC   sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC   sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC   deleted), a construct useful in the treatment of cancer comprising a
CC   superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell
CC   useful in the treatment of cancer (where an adaptor protein which
CC   inhibits T cell activation by tumour associated antigens is deleted or
CC   functionally deactivated), a composition useful in the treatment of
CC   cancer (comprising a lipid raft conjugated to a superantigen), producing
CC   (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC   allowing tumour associated lipids to contact immunocytes, in which
CC   receptors for the lipids are inactivated or deleted to produce a
CC   tumouricidal immunocyte population, and administering the tumouricidally
CC   activated immunocytes to the host), producing (M3) a tumouricidal APC
CC   population ex vivo in a mammal (by allowing a tumour associated lipid to
CC   contact APCs, in which receptors for the tumour associated lipids are
CC   inactivated or deleted to produce a tumouricidally activated population,
CC   and administering APCs to the host), producing a tumouricidal T cell
CC   population ex vivo in a mammal) by allowing a tumour associated lipids to
CC   contact T cells, in which adaptor proteins, which inhibit T cell
CC   activation by tumour associated antigens, are deleted or functionally
CC   deactivated to produce a tumouricidal population of T cells, and
CC   administering the tumouricidally activated T cells to the host, or
CC   allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC   administering the tumouricidally activated T cells to the host), treating
CC   (M5) cancer in a mammal (by administering a lipid binding molecule which
CC   binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC   a tumouricidal T cell population in vivo in a mammal (by allowing a
CC   tumour associated antigen to contact immunocytes in which adaptor
CC   proteins which inhibit T cell activation by tumour associated antigens
CC   are deleted or functionally deactivated) and producing (M7) a
CC   tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC   superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC   receptors, methods and compositions are useful for treating cancers and
CC   tumours. Bacterial superantigens are co-administered or administered as
CC   fusion constructs with anti-tumour proteins or motifs. The present
CC   sequence encodes an anti-tumour protein which is co-administered with or
CC   incorporated into a fusion construct with a superantigen. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from the US patnet
CC   office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-106      Length:          1156
Score:                  1493.00        Matches:         299
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     8              Gaps:            0

US-09-827-854A-2 (1-299) x ACA64743 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 10
ACC49103
ID   ACC49103 standard; cDNA; 1156 BP.
XX
AC   ACC49103;
XX
DT   18-JUN-2003  (first entry)
XX
DE   Human apolipoprotein E coding region nucleotide sequence.
XX
KW   Human; apolipoprotein E; apoE; haplotype; detection; allele; genotype;
KW   multiple haplotypic genetic variation; polymorphism; chromosome 19q13.2;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003018835-A2.
XX
PD   06-MAR-2003.
XX
PF   22-AUG-2002; 2002WO-DK000552.
XX
PR   23-AUG-2001; 2001DK-00001252.
XX
PA   (HVID-) HVIDOVRE HOSPITAL.
XX
PI   Fenger M,  Bentzen J;
XX
DR   WPI; 2003-342453/32.
XX
PT   Determining the genetic haplotype of a part of an individual genotype,
PT   comprises determining the presence or absence of specific nucleotide
PT   polymorphisms of a pair of homologous chromosomes.
XX
PS   Example 3; Page; 56pp; English.
XX
CC   The present invention describes a method for detecting the presence or
CC   absence of multiple haplotypic genetic variations in a preselected region
CC   of one chromosome of a chromosome pair comprises selecting nucleotide
CC   polymorphisms, suspected to occur in the preselected region, isolating a
CC   target nucleic acid (TNA) of the chromosome pair from a sample, and
CC   detecting the presence or absence of several polymorphisms, using
CC   designed oligonucleotide probes. The method is useful for detecting the
CC   presence or absence of multiple haplotypic genetic variations in a
CC   preselected region of one chromosome of a chromosome pair. The method is
CC   also useful for determining the linkage phase between two adjacent loci.
CC   The method is fast, inexpensive and provides uncomplicated determination
CC   of haplotypes in nucleic acid fragments of varying length from 25-40000
CC   base pairs. The present sequence represents the human apolipoprotein E
CC   (apoE) coding region nucleotide sequence, which is used in the
CC   exemplification of the present invention. Human apoE is located on
CC   chromosome 19q13.2. N.B. The present sequence is not given in the
CC   specification, but the coding sequence of apoE is referred to in Example
CC   3 by Genbank accession number K00396
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.13e-106      Length:          1156
Score:                    1493.00        Matches:         299
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              100.0%         Indels:          0
DB:                       8              Gaps:            0

US-09-827-854A-2 (1-299) x ACC49103 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 11
ACC84919
ID   ACC84919 standard; DNA; 1156 BP.
XX
AC   ACC84919;
XX
DT   03-OCT-2003  (first entry)
XX
DE   Human apo E polypeptide encoding DNA.
XX
KW   Nuclear hormone receptor ligand; ophthalmological; cholesterol transport;
KW   lipid efflux; macular degeneration; apolipoprotein E; apo E; human; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             61. .1014
FT                   /*tag=  a
FT                   /product= "Apo E"
XX
PN   WO2003049685-A2.
XX
PD   19-JUN-2003.
XX
PF   06-DEC-2002; 2002WO-US038856.
XX
PR   07-DEC-2001; 2001US-0340498P.
PR   03-OCT-2002; 2002US-0415864P.
XX
PA   (SCHW/) SCHWARTZ D M.
PA   (DUNC/) DUNCAN K.
PA   (BAIL/) BAILEY K.
PA   (KANE/) KANE J.
PA   (ISHI/) ISHIDA B.
XX
PI   Schwartz DM,  Duncan K,  Bailey K,  Kane J,  Ishida B;
XX
DR   WPI; 2003-586846/55.
DR   P-PSDB; ABR62030.
XX
PT   Increasing lipid efflux from and reverse cholesterol transport in ocular
PT   tissue used for treating e.g. macular degeneration comprises delivering
PT   nuclear hormone receptor ligand.
XX
PS   Disclosure; Page 55-56; 97pp; English.
XX
CC   The invention relates to increasing lipid efflux from and reverse
CC   cholesterol transport in an ocular tissue and involves delivering at
CC   least one nuclear hormone receptor ligand. The method is used for
CC   increasing lipid efflux and reverse cholesterol transport in ocular
CC   tissue, preferably retinal pigment epithelium (RPE) and/or Bruch's
CC   membrane, in an individual afflicted with AMD or Stargardts disease
CC   (fundus flavimaculatus), and for treating macular degeneration. The
CC   present sequence represents a DNA encoding a human apolipoprotein E (Apo
CC   E) (GenBank Accession No. K00396)
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-106       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     9               Gaps:           0

US-09-827-854A-2 (1-299) x ACC84919 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 12
ADA14198
ID   ADA14198 standard; cDNA; 1156 BP.
XX
AC   ADA14198;
XX
```

DT 06-NOV-2003 (first entry)
XX
DE Human apolipoprotein E (ApoE) encoding cDNA SEQ ID NO:1.
XX
KW identification; fluorescence resonance energy transfer; FRET;
KW single nucleotide polymorphism; SNP; mutation; nucleic acid polymerase;
KW nucleic acid sequencing; human; apolipoprotein E; ApoE;
KW chromosome 19q13.2; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61. .1014
FT /*tag= a
FT /product= "apolipoprotein E (ApoE)"
XX
PN WO2003068986-A1.
XX
PD 21-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-EP050013.
XX
PR 11-FEB-2002; 2002EP-00100124.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Turcatti G;
XX
DR WPI; 2003-679643/64.
DR P-PSDB; ADA14199.
XX
PT Identifying a nucleotide in a nucleic acid by means of Fluorescence
PT Resonance Energy Transfer by monitoring the presence or absence of
PT incorporation of the nucleotide chemically linked to the second FRET-
PT generating fluorophore.
XX
PS Example 1; Page 50-51; 59pp; English.
XX
CC The present invention describes a method (M1) for identifying a
CC nucleotide in a nucleic acid by means of fluorescence resonance energy
CC transfer (FRET). M1 comprises: (a) providing a first nucleic acid
CC containing the nucleotide to be identified in a single-stranded
CC conformation at least in the portion including the nucleotide to be
CC identified and the sequence immediately in 3' to the nucleotide; (b)
CC providing a second nucleic acid comprising a single-stranded 3' end
CC complementary to the sequence of the first nucleic acid immediately in 3'
CC to the nucleotide to be identified, and a first FRET-generating
CC fluorophore linked to a nucleotide located from 1-12 nucleotides far
CC apart from the 3' terminal nucleotide of the second nucleic acid; (c)
CC hybridising the first and second nucleic acid, resulting in a nucleic
CC acid, where the sequence immediately in 3' to the nucleotide is in the
CC double stranded conformation; (d) adding the nucleic acid polymerase and
CC at least a nucleotide chemically linked to a second FRET-generating
CC fluorophore; (e) allowing the nucleic acid polymerase to perform a single
CC base extension at the 3' end of the first nucleic acid; and (f)
CC monitoring the incorporation, or the absence of incorporation, of the
CC nucleotide chemically linked to the second FRET-generating fluorophore
CC using a FRET-based analytical technology. Also described: (1) identifying
CC a single nucleotide polymorphism (SNP) or mutation; (2) evaluating the
CC extension of properties of nucleic acid polymerases, or the preference of
CC nucleic acid polymerases for the same nucleotide when labelled or non-
CC labelled by employing M1; (3) screening modulators of nucleic acid
CC polymerases by employing M1; (4) sequencing nucleic acids according to M1
CC ; and (5) kits, useful for the methods described above, comprising at
CC least a nucleic acid having an internal nucleotide located from 1-12
CC nucleotides far apart from the 3' terminal nucleotide linked to a first
CC FRET-generating fluorophore polymerase and at least a nucleotide
CC chemically linked to a second FRET-generating fluorophore. The methods
CC and kits of the present invention are useful for identifying a SNP or
CC mutation, evaluating the extension of properties of nucleic acid
CC polymerases or the preference of nucleic acid polymerases for the same
CC nucleotide when labelled or non-labelled, screening modulators of nucleic
CC acid polymerases by employing the novel method, and sequencing nucleic
CC acids. The present sequence encodes human apolipoprotein E (ApoE), which
CC is used in an example from the present invention. Human ApoE is located
CC on chromosome 19q13.2.
XX
SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-106	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-09-827-854A-2 (1-299) x ADA14198 (1-1156)

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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 13
ADF43409
ID   ADF43409 standard; DNA; 1156 BP.
XX
AC   ADF43409;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Apolipoprotein polynucleotide seqid 129.
XX
KW   receptor; lipid-based tumour associated antigen; cytostatic;
KW   antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW   infectious disease; apolipoprotein; ds.
XX
OS   Unidentified.
XX
PN   US2003157113-A1.
XX
PD   21-AUG-2003.
XX
PF   28-DEC-2000; 2000US-00751708.
XX
PR   28-DEC-1999;   99US-0173371P.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2003-787326/74.
DR   P-PSDB; ADF43410.
XX
PT   New receptor in a mammalian cell that inhibits regular activation by
PT   receptors specific for lipid-based tumor associated antigens, useful for
PT   treating a neoplastic disease or tumor, and infectious diseases.
XX
PS   Example 3; SEQ ID NO 129; 151pp; English.
XX
CC   The invention describes a receptor in a mammalian cell that inhibits
CC   regular activation by receptors specific for lipid-based tumour
CC   associated antigen. The receptor has cytostatic and antimicrobial
CC   properties and is suitable for use in gene therapy. The receptors,
CC   methods and compositions are useful for treating a neoplastic disease or
CC   tumour (cancer), and infectious diseases. This sequence represents
CC   apolipoprotein polynucleotide, a cell surface moiety, the DNA of which
CC   can be transfected into a cell with superantigen DNA to generate
CC   antitumour immunity.
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-106      Length:         1156
Score:                  1493.00        Matches:        299
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     10             Gaps:           0

US-09-827-854A-2 (1-299) x ADF43409 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 14
ADI31681
ID   ADI31681 standard; cDNA; 1156 BP.
XX
AC   ADI31681;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human cDNA #1007.
XX
KW   Human; gene; ss; immunological response; immunopathological condition;
KW   Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW   irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW   acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW   osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US6607879-B1.
XX
PD   19-AUG-2003.
XX
PF   09-FEB-1998;   98US-00023655.
XX
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PR   09-FEB-1998;   98US-00023655.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Cocks BG,  Stuart SG,  Seilhamer JJ;
XX
DR   WPI; 2003-895307/82.
XX
PT   A composition comprising a plurality of cDNAs, useful for detecting
PT   altered expression of genes in an immunological response or for
PT   diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT   or osteoarthritis.
XX
PS   Claim 1; SEQ ID NO 1007; 50pp; English.
XX
CC   The invention relates to a composition comprising a plurality of cDNAs
CC   for detecting the altered expression of genes in an immunological
CC   response. The invention also relates to a method of diagnosing or
CC   monitoring the treatment of an immunopathological condition in a sample,
CC   comprising obtaining nucleic acids from a sample, contacting the nucleic
CC   acids of the sample with an array comprising the plurality of cDNAs under
CC   conditions to form one or more hybridisation complexes, detecting the
CC   hybridisation complexes and comparing the levels of the detected
CC   hybridisation complexes with the level of hybridisation complexes
CC   detected in a non-diseased sample, where an altered level of the detected
CC   hybridisation complexes correlates with the presence of an
CC   immunopathological condition. Also disclosed are an expression profile
CC   comprising a microarray and a plurality of detectable complexes and a
CC   method for identifying a plurality of polynucleotide probes. The cDNAs
CC   are useful as hybridisable array elements in a microarray for monitoring
CC   the expression of target polynucleotides. The microarray can be used in
CC   the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC   ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC   osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC   identifying agents for the treatment of the diseases. The microarray may
CC   also be used in drug discovery and development, toxicological and
CC   carcinogenicity studies, forensics or pharmacogenomics. The composition
CC   may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC   genomic fragments. This sequence represents a human cDNA of the
CC   invention. Note: The sequence data for this patent did not form part of
CC   the printed specification but was obtained in electronic format directly
CC   from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.13e-106       Length:          1156
Score:                    1493.00         Matches:         299
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       11              Gaps:            0

US-09-827-854A-2 (1-299) x ADI31681 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 15
AEB86465
ID   AEB86465 standard; DNA; 1156 BP.
XX
AC   AEB86465;
XX
DT   06-OCT-2005  (first entry)
XX
DE   Human apolipoprotein E encoding DNA.
XX
KW   selectable marker; osteopathic; antiarthritic; diagnosis; osteoarthritis;
KW   cartilage damage; fractures; gene; ds; apolipoprotein E.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             61. .1014
FT                   /*tag=  a
FT                   /product= "Human apolipoprotein E"
XX
PN   JP2003225093-A.
XX
PD   12-AUG-2003.
XX
PF   29-NOV-2002; 2002JP-00348073.
XX
PR   30-NOV-2001; 2001JP-00367993.
XX
PA   (SUMU ) SUMITOMO SEIYAKU KK.
XX
DR   WPI; 2003-703023/67.
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DR   P-PSDB; AEB86466.
XX
PT   Marker for screening for compounds influencing a gene or protein, for
PT   treating cartilage disorders, such as, osteoarthritis, comprises a
PT   polynucleotide or a complement to specific genes, or an antibody to its
PT   protein.
XX
PS   Claim 1; SEQ ID NO 13; 64pp; Japanese.
XX
CC   The invention relates to a novel marker for cartilage disorders. The
CC   marker consists of a polynucleotide sequence of 15 bases from the
CC   sequence of acetyl-Coenzyme A acetyltransferase 1, Rev-ErbA-beta,
CC   Selenoprotein P, aquaporin 1, BMP-3b; FK506-binding protein 1A,
CC   apolipoprotein E, acyl-CoA synthetase 5, epoxide hydrolase 1, or
CC   glutamine synthase gene, and/or a polynucleotide complementary to one of
CC   these. The invention further comprises: a detection method of a cartilage
CC   disorder; a disease marker for cartilage disease containing an antibody
CC   to the amino acid, as given in the specification; a detection method of a
CC   cartilage disorder using a protein sample from the subject, or a peptide
CC   from it, and the antibody as a label; screening for a material which
CC   controls expression of one of the genes above; screening for a material
CC   which controls the activity or function of one of the proteins; and an
CC   agent to improve or treat a cartilage disorder which contains a substance
CC   controlling expression of the genes or activity of the proteins. The
CC   novel marker has osteopathic and antiarthritic activities. The markers
CC   may be used as a probe or a primer, for diagnosis of conditions such as
CC   osteoarthritis, chondrodystrophy, discopathy, cartilage damage, semilunar
CC   cartilage disorder, deficient healing of fractures, or in chondrocyte
CC   transplants. The screening methods are useful for identifying therapeutic
CC   compounds. This polynucleotide sequence represents the DNA encoding
CC   apolipoprotein E of the invention.
XX
SQ   Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.13e-106      Length:          1156
Score:                  1493.00        Matches:         299
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            100.0%         Indels:          0
DB:                     11             Gaps:            0

US-09-827-854A-2 (1-299) x AEB86465 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

Search completed: June 14, 2006, 19:10:42
Job time : 1035.05 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:39 ; Search time 7915.48 Seconds
(without alignments)
3168.451 Million cell updates/sec

Title: US-09-827-854A-2
Perfect score: 1493
Sequence: 1 KVEQAVETEPEPELRQQTEW.....VEKVQAAVGTSAAPVPSDNH 299

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09827854/runat_14062006_081827_26762/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US09827854_@CGN_1_1_7986_@runat_14062006_081827_26762 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1211	81.1	975	8	CO580643	CO580643 ILLUMIGEN
2	1209	81.0	937	8	CO775017	CO775017 ILLUMIGEN
3	1198.5	80.3	1027	2	BI670367	BI670367 603292738
4	1162	77.8	842	2	BG763371	BG763371 602735433
5	1156	77.4	933	2	BI668318	BI668318 603295681
6	1142	76.5	786	8	CX165559	CX165559 HESC2_30_
7	1137.5	76.2	909	3	BU849868	BU849868 AGENCOURT
8	1128	75.6	938	2	BG761746	BG761746 602717942
9	1125.5	75.4	942	2	BI600906	BI600906 603249241
c 10	1123	75.2	834	2	BM042676	BM042676 603616028
11	1111	74.4	800	2	BM042094	BM042094 603615713
12	1110.5	74.4	927	2	BG472299	BG472299 602513830
13	1107.5	74.2	922	2	BI597743	BI597743 603248609
14	1104	73.9	706	3	BM728696	BM728696 UI-E-EJ0-
c 15	1099	73.6	954	2	BF967543	BF967543 602287404
16	1098.5	73.6	817	2	BG774871	BG774871 602649975
17	1097	73.5	811	2	BI600563	BI600563 603244936
18	1096	73.4	1087	6	BC044785	BC044785 Mus muscu
19	1092	73.1	1109	6	AK159517	AK159517 Mus muscu
20	1092	73.1	1111	6	AK134921	AK134921 Mus muscu
21	1092	73.1	1111	6	AK159105	AK159105 Mus muscu
22	1089	72.9	1094	6	AK149568	AK149568 Mus muscu
23	1088	72.9	1111	6	AK159424	AK159424 Mus muscu
24	1083.5	72.6	845	2	BG829472	BG829472 602763768
25	1083	72.5	948	3	BU194461	BU194461 AGENCOURT
26	1082.5	72.5	861	9	DN102220	DN102220 1097106 M
c 27	1082.5	72.5	930	2	BF967857	BF967857 602287176
28	1081	72.4	1111	6	AK150834	AK150834 Mus muscu
29	1078	72.2	688	2	BI544886	BI544886 603242328
30	1077	72.1	1271	10	DV789745	DV789745 HW_LIVER_
31	1076	72.1	831	10	DR772634	DR772634 ILLUMIGEN
32	1073	71.9	1110	6	AK010261	AK010261 Mus muscu
c 33	1072	71.8	816	4	CA307890	CA307890 UI-H-FT1-
34	1069	71.6	1269	10	DV782549	DV782549 Hw_liver_
35	1060	71.0	790	2	BG707147	BG707147 602670283
36	1057	70.8	919	2	BI551475	BI551475 603194314
37	1055.5	70.7	909	3	BU190668	BU190668 AGENCOURT
38	1052	70.5	1273	6	AK131624	AK131624 Mus muscu
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c 40	1050	70.3	858	2	BF967549	BF967549 602287410
41	1047	70.1	757	2	BM042228	BM042228 603616186
42	1044.5	70.0	936	3	BU859124	BU859124 AGENCOURT
43	1039	69.6	711	2	BM041876	BM041876 603615933
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45	1037.5	69.5	907	2	BG706129	BG706129 602669093

ALIGNMENTS

RESULT 1
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LOCUS CO580643 975 bp mRNA linear EST 20-JUL-2004
DEFINITION ILLUMIGEN_MCQ_48393 Katze_MMLV Macaca mulatta cDNA clone IBIUW:18409 5' similar to Bases 755 to 975 highly similar to human Unigene Hs.515465, mRNA sequence.
ACCESSION CO580643
VERSION CO580643.1 GI:50411831
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 975)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B., Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com

```
          Sequenced on 2004.07.02. 690 Q20 bases. Library Preparation: Prof.
          Michael Katze Lab at University of Washington DNA Sequencing:
          Illumigen Biosciences Inc. For further information, see
          http://www.macaque.org
          PCR PRimers
          FORWARD: CCCTCACTAAAGGGAACAAAA
          BACKWARD: CACTATAGGGCGAATTGGGTA
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                    /clone_lib="Katze_MMLV"
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                    Site_2: BsrG I; Created from CloneMiner cDNA Library
                    Construction kit (catalog #18249-029)"
ORIGIN

Alignment Scores:
Pred. No.:              1.22e-105      Length:         975
Score:                  1211.00        Matches:        254
Percent Similarity:     88.3%          Conservative:   9
Best Local Similarity:  85.2%          Mismatches:     34
Query Match:            81.1%          Indels:         1
DB:                     8              Gaps:           0

US-09-827-854A-2 (1-299) x CO580643 (1-975)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||   ||||||   |||   ||||||||||||||||||||   |||
Db         84 AAGGTGGAGCAACCGGTGGAGCCAGAGACGGAACCCGAGCTTCGCCAGCAGGCTGAGGGG 143

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        144 CAGAGCGGCCAGCCCTGGGAGCTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 203

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        204 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCCCCCAGGTCACCCAGGAACTG 263

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Db        264 ACGACGCTGATGGATGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 323

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        324 CAGCTGAGCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 383

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Db        384 CAGGCCCGGCTGGGTGCCGACATGGAGGACGTGCGCAGCCGCCTGGTGCAGTACCGCAGC 443

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        444 GAGGTGCAGGCCATGCTGGGCCAGAGTACCGAGGAGCTGCGGGCGCGCCTCGCCTCCCAC 503

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        504 CTGCGCAAGCTGCGCAAGCGGCTCCTCCGCGATGCTGATGACCTGCAGAAGCGCCTGGCA 563

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        564 GTGTATCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGGGTCAGCGCCATCCGCGAGCGC 623

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db        624 CTGGGACCCCTGGTGGAGCAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCAGC 683

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Db        684 CAGCCGCTTCAGGAGCGGGCCCAGGCCTTGAGTGAGCGGCTTCGCGCACGGATGGAGGAA 743

Qy        221 MetGlySerArgThrArgAsp-ArgLeuAspGluValLysGluGlnValAlaGluValAr 240
              ||||||||||||||||||::: ||||||||||||||||||||||||||||||||||||
Db        744 ATGGGCAGCCGGACCCGCGAACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAAGTGCG 803

Qy        240 gAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaAr 260
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Qy        260 gLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVa 280
              |   |||:::||||||:::||||||   :::            :::   |||||||||
Db        864 CTTCAAAAACTGGTTCCAGCCCCTGGGGAAAAAATGGCACCCCCGTGGGGCTGGGCTGGG 923

Qy        280 lGluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAsp 297
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Db        924 GGAAAAAGGGCAAGGTGCCCGGGGCGCCCACCCCCCCCCCTGGCCCAACGAC 975

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CO775017
LOCUS       CO775017                937 bp    mRNA    linear   EST 04-AUG-2004
DEFINITION  ILLUMIGEN_MCQ_52207 Katze_MNLV Macaca nemestrina cDNA clone
            IBIUW:28964 5' similar to Bases 5 to 934 highly similar to human
            APOE (Hs.110675), mRNA sequence.
ACCESSION   CO775017
VERSION     CO775017.1  GI:50976280
KEYWORDS    EST.
SOURCE      Macaca nemestrina (pig-tailed macaque)
  ORGANISM  Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 937)
  AUTHORS   Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
            Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
            Iadonato,S.P.
  TITLE     Analysis of the Macaca mulatta transcriptome and the sequence
            divergence between Macaca and human
  JOURNAL   Genome Biol. 6 (7), R60 (2005)
   PUBMED   15998449
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.21. 706 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR PRimers
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                    /sex="male"
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/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I; Site_2: BsrG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.:	1.8e-105	Length:	937
Score:	1209.00	Matches:	253
Percent Similarity:	91.2%	Conservative:	5
Best Local Similarity:	89.4%	Mismatches:	24
Query Match:	81.0%	Indels:	1
DB:	8	Gaps:	0

US-09-827-854A-2 (1-299) x CO775017 (1-937)

```
Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||   ||||||   |||   ||||||||||||||||||||   |||
Db         84 AAGGTGGAGCAACCGGTGGAGCCAGAGACGGAACCCGAGCTTCGCCAGCAGGCTGAGGGG 143

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        144 CAGAGCGGCCAGCCCTGGGAGCTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 203

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        204 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCCCCCAGGTCACCCAGGAACTG 263

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db        384 CAGGCCCGGCTGGGTGCCGACATGGAGGACGTGCGCAGCCGCCTGGTGCAGTACCGCAGC 443

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        444 GAGGTGCAGGCCATGCTGGGCCAGAGTACCGAGGAGCTGCGGGCGCGCCTCGCCTCCCAC 503

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        504 CTGCGCAAGCTGCGCAAGCGGCTCCTCCGCGATGCTGATGACCTGCAGAAGCGCCTGGCA 563

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        564 GTGTATCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGGGTCAGCGCCATCCGCGAGCGC 623

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGGGACCCCTGGTGGAGCAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCAGC 683

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        684 CAGCCGCTTCAGGAGCGGGCCCAGGCCTTGGGTGAGCGGCTTCGCGCACGGATGGAGGAG 743

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAAGAACAGGTGGCGGAGGTGCGC 803

Qy        241 AlaLysLeuGlu-GluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaAr 260
              ||||||||||| |||||||||      |||   ||||||||||||||||||||||||||
Db        804 GCCAAGCTGGAAGGAACAGGCCCACCATATAAGCCTGCAGGCCGAGGCCTTCCAGGCCCG 863

Qy        260 gLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVa 280
              |   ::::::||||||:::||||||||||||   |||   |||      |||||||||
Db        864 CCCCCAAAACTGGTTCAAGCCCCTGGTGGAAAAAATGGACCGCCCGGGGGCTGGGCTTGG 923

Qy        280 lGluLys 282
               |||||||
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Db 924 TGAAAAA 930

RESULT 3
BI670367
LOCUS BI670367 1027 bp mRNA linear EST 12-SEP-2001
DEFINITION 603292738F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312024 5', mRNA sequence.
ACCESSION BI670367
VERSION BI670367.1 GI:15584600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11790 row: 1 column: 09
High quality sequence stop: 845.

FEATURES Location/Qualifiers
source 1. .1027
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5312024"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.06e-104	Length:	1027
Score:	1198.50	Matches:	274
Percent Similarity:	90.3%	Conservative:	6
Best Local Similarity:	88.4%	Mismatches:	19
Query Match:	80.3%	Indels:	12
DB:	2	Gaps:	2

US-09-827-854A-2 (1-299) x BI670367 (1-1027)

```
Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 139

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 199

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 259
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```
Qy          61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         260 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 319

Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         320 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCAAAGGAGCTGCAGGCGGCG 379

Qy         101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         380 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 439

Qy         121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         440 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 499

Qy         141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         500 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 559

Qy         161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         560 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 619

Qy         181 Leu-GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGl 200
               ||| ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         620 CTGGGGCCCCCTGGTGGAACAGGTCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGG 679

Qy         200 yGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArg-LeuArgAlaArgMetGluG 220
               ||||||||||||||||||||:::|||||||||||||||| ||||||||||||||||||||
Db         680 CCAGCCGCTACAGGAGCGGGCCAAGGCCTGGGGCGAGCGGCTTGCGCGCGCGGATGGAGG 739

Qy         220 lu-MetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu-V 239
               ||    |||||||| ||||||||||||      |||||||||||||||||||||||| |
Db         740 AAGAGGGGCAGCCGGGACCCGCGACCGCTGGACCGAGGTGAAGGAGCAGGTGGCGGAAGG 799

Qy         239 alArgAlaLysLeu---GluGluGlnAlaGlnGln-IleArgLeuGln-AlaGluAlaPh 257
               |||||||:::            |||||||||||| |||||||||||| |||||||||
Db         800 TGCGCGCCCAAGCTGGACGGAGCCAGGCCCAGCAAGATACGCCTGCAGGGCCGAGGCTTC 859

Qy         257 eGlnAlaArgLeuLysSerTrpPheGluPro------LeuValGluAspMetGlnArgGl 275
                 |||||   :::|||||||||||||||      |||          :::|||||
Db         860 CTAGGCCCGGCCTCAGAGCTGGTTCGAACCCCCTGGGTTGGAACGACATGGCCGGCGCCA 919

Qy         275 nTrpAlaGlyLeuValGluLysVal-GlnAlaAlaValGlyThrSerAlaAlaProValP 295
               ||||||||||      :::|||||| |||||||||   ||||||:::|||||   ||||
Db         920 GTGGGCCGGCTGGTGGAAAAAGGTGCCAGGCTGCCGGGGGCACCACCGCCGCCCTGGTGC 979

Qy         295 roSerAspAsnHis 299
               ||   |||||||||
Db         980 CAGC-GACAATCAT 992

RESULT 4
BG763371
LOCUS       BG763371                842 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602735433F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4860585 5',
            mRNA sequence.
ACCESSION   BG763371
VERSION     BG763371.1  GI:14074024
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 842)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1718  row: b  column: 10
           High quality sequence stop: 817.
FEATURES             Location/Qualifiers
     source          1. .842
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4860585"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_49"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
ORIGIN

Alignment Scores:
Pred. No.:                5.06e-101      Length:          842
Score:                    1162.00        Matches:         242
Percent Similarity:       96.8%          Conservative:    2
Best Local Similarity:    96.0%          Mismatches:      7
Query Match:              77.8%          Indels:          2
DB:                       2              Gaps:            0

US-09-827-854A-2 (1-299) x BG763371 (1-842)

Qy           1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          90 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 149

Qy          21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         150 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 209

Qy          41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         210 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 269

Qy          61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         270 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 329

Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         330 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 389

Qy         101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         390 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 449

Qy         121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         450 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 509

Qy         141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         510 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 569

Qy         161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         570 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 629
```

```
Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CTGGGGCCCTG-GTGGAACAGGGCCGCGTGCGGGCCGCAACTGTGGGCTCCCTGGCCGGC 688

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 748

Qy        221 Met-GlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValAr 240
              ||| ||||||||||||||||||||          ::::::||||||||||||||||||
Db        749 ATGCGGCAGCCGGACCCGCGACCGCTGGACGAGGTGAAGGGACCAGGTGGCGGAGGTGCG 808

Qy        240 gAlaLysLeuGluGluGlnAlaGlnGlnIleArg 251
              ||||      ||||||||||||||||||||||||
Db        809 CGCAAGCTGGGAGGAGCAGGCCCAGCAGATACGC 842
```

RESULT 5
BI668318

```
LOCUS       BI668318                933 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603295681F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314844 5',
            mRNA sequence.
ACCESSION   BI668318
VERSION     BI668318.1  GI:15582551
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11798  row: a  column: 21
            High quality sequence stop: 780.
FEATURES             Location/Qualifiers
     source          1. .933
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5314844"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              2.17e-100       Length:         933
Score:                  1156.00         Matches:        245
Percent Similarity:     93.7%           Conservative:   7
Best Local Similarity:  91.1%           Mismatches:     14
Query Match:            77.4%           Indels:         4

DB:                     2               Gaps:           1

US-09-827-854A-2 (1-299) x BI668318 (1-933)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 188

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 248

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 308

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 368

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 428

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 488

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 548

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 608

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 668

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 728

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArg-MetGlu-- 219
              |||||||||||||||||||||||||||||||||||||||||||||||||| :::|||
Db        729 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATTGGAGGC 788

Qy        220 -GluMetGlySerArgThrArgAspArgLeuAsp-GluValLysGluGlnValAlaGluV 239
               |||||||||||||||:::|||||::: |||||||||||||||||||   ::::
Db        789 ACATTGGGGCAGCCGGACCCGCGAACGCCTGGAACGAGGTGAAGGAGCAGGTGCGGAAGT 848

Qy        239 alArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnA 259
              ::|||   :::                     ||||||||||||||   ||||||||||
Db        849 TGCGCCGCCAAGGCTGGGGGACCAGGCCCGCAATTCGCTTGCAGGCCAA-GCCTTCCAGG 907

Qy        259 laArgLeuLysSerTrpPheGlu 266
              ||      ||||||||||||:::
Db        908 CCGGCTCCAAGAGCTGGTTCAAA 930
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RESULT 6
CX165559

```
LOCUS       CX165559                786 bp    mRNA    linear   EST 23-DEC-2004
DEFINITION  HESC2_30_A09.g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
            IMAGE:7469084 5', mRNA sequence.
ACCESSION   CX165559
VERSION     CX165559.1  GI:56795639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

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REFERENCE   1  (bases 1 to 786)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
             cDNA Library Preparation: Express Genomics, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15769  row: a  column: 18
            Seq primer: JENREV (CAGGAAACAGCTATGACC)
            High quality sequence stop: 786.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7469084"
                     /sex="male"
                     /tissue_type="human embryonic stem cells differentiated to
                     an early endodermal cell type"
                     /cell_type="human embryonic stem cells"
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                     /lab_host="DH10B-T1 phage-resistant E. coli"
                     /clone_lib="NIH_MGC_258"
                     /note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
                     RNA obtained from human embryonic stem cells isolated from
                     the inner cell mass of blastocyst stage embryos and
                     differentiated to an early endodermal cell type. Cell line
                     id and NIH Registry designation is BG01. Positive for
                     GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP
                     expression. Passage number 40. cDNA primed using oligo-dT
                     primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and
                     cloned into the EcoRV/NotI sites of pExpress-1. This
                     primary library is non-normalized (normalized primary
                     library is NIH_MGC_259). It was constructed by Express
                     Genomics (Frederick, MD). Sequence ends have been trimmed
                     to exclude vector and regions below Phred quality 16.
                     Three-prime sequences are presented as their reverse
                     complement and have been trimmed to exclude polyA. Note:
                     this is a Mammalian Gene Collection library."
ORIGIN

Alignment Scores:
Pred. No.:                3.84e-99        Length:          786
Score:                    1142.00         Matches:         229
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              76.5%           Indels:          0
DB:                       8               Gaps:            0

US-09-827-854A-2 (1-299) x CX165559 (1-786)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 159

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 219

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 279

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 339

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 399

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 459

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 519

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 579

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 639

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 699

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 759

Qy        221 MetGlySerArgThrArgAspArgLeu 229
              |||||||||||||||||||||||||||
Db        760 ATGGGCAGCCGGACCCGCGACCGCCTG 786

RESULT 7
BU849868
LOCUS       BU849868                909 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10440638 NIH_MGC_109 Homo sapiens cDNA clone
            IMAGE:6598569 5', mRNA sequence.
ACCESSION   BU849868
VERSION     BU849868.1  GI:24034831
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 909)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2831  row: j  column: 09
            High quality sequence stop: 574.
FEATURES             Location/Qualifiers
     source          1. .909
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6598569"
                     /tissue_type="teratocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_109"
```

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                  /note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
                  XhoI; cDNA made by oligo-dT priming.  Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGCACGAG(G).  Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.25e-98        Length:         909
Score:                  1137.50         Matches:        242
Percent Similarity:     90.8%           Conservative:   6
Best Local Similarity:  88.6%           Mismatches:     19
Query Match:            76.2%           Indels:         6
DB:                     3               Gaps:           1

US-09-827-854A-2 (1-299) x BU849868 (1-909)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 154

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 214

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 274

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 334

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 394

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 454

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 514

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 574

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 634

Qy        181 Leu-GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGl 200
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        635 CTGGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGGCGG 694

Qy        200 yGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArg---MetGl 219
              |||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db        695 CCAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGGCGAGCGGCTGCCCCCCGCGGGATGGA 754

Qy        219 uGluMetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu- 238
              ||||||||||:::||| |||     ||||||:::::::||||||:::|||||||||||||
Db        755 AGAGATGGGCAACCGGAACCCCGCACCGCCTGGAAAAGGTGAAGGACCAGGTGGCGGAAG 814

Qy        239 -ValArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGl 258
                   |||||||||        |||   |||||||||   |||   |||||
Db        815 GTGCCCCCCCAGCCTGGAGGAAGCAGGCCCACAAAAACGCCTGCAGGGCGAGGGCTTCCA 874

Qy        258 n-AlaArgLeuLysSerTrpPheGluPro 267
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              | ||||||   |||:::||||||:::|||
Db        875 GGGCCCGCTTCAAGAACTGGTTCCAGCCC 903

RESULT 8
BG761746
LOCUS       BG761746                938 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602717942F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4841411 5',
            mRNA sequence.
ACCESSION   BG761746
VERSION     BG761746.1  GI:14072399
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 938)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1674  row: c  column: 12
            High quality sequence stop: 767.
FEATURES             Location/Qualifiers
     source          1. .938
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4841411"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_49"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
ORIGIN

Alignment Scores:
Pred. No.:              1.06e-97        Length:         938
Score:                  1128.00         Matches:        254
Percent Similarity:     92.1%           Conservative:   4
Best Local Similarity:  90.7%           Mismatches:     11
Query Match:            75.6%           Indels:         11
DB:                     2               Gaps:           2

US-09-827-854A-2 (1-299) x BG761746 (1-938)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 170

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 230

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 290
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Qy          61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         291 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 350

Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         351 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 410

Qy         101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         411 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 470

Qy         121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         471 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 530

Qy         141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         531 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 590

Qy         161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
               ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         591 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGTGCTCAGCGCCATCCGCGAGCGC 650

Qy         181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySer-LeuAlaGl 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         651 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTTGGCCGG 710

Qy         200 yGlnProLeuGlnGluArgAlaGlnAlaTrp-GlyGluArg-LeuArgAlaArgMetGlu 219
               ||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db         711 CCAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGGCGAGCGGCTTGCGCGCGCGGATGGAG 770

Qy         220 ---GluMetGlySerArgThr-Arg-AspArgLeuAspGluValLys-GluGlnValAla 237
                  :::|||||| ||| ||||||||||||||||||| ||||||||||||
Db         771 GGACATTGGGCAGCCCGGACCCCGGCGACCGCTTGGACGAGGTGAAGGGAGCAGGTGGCG 830

Qy         238 ---GluValArgAlaLysLeuGluGlu-GlnAlaGlnGlnIleArgLeuGlnAla--Glu 255
                     :::   |||||||||||||||| |||   |||:::|||||||||||||||  :::
Db         831 GGAAGGTTGGGCGCCAAGCTGGAGGAAGCAGGGCCAGGAGATACGCCTGCAGGCCGGAAG 890

Qy         256 AlaPheGlnAlaArgLeuLysSerTrpPheGluProLeuVal 269
               |||      ||||||||||||||||||||   ||||||
Db         891 GGCTTCCCAGGCCGGCTCAAAAGCTGGTTCGAAGCCCTGGTT 932

RESULT 9
BI600906
LOCUS       BI600906                942 bp    mRNA    linear   EST 07-SEP-2001
DEFINITION  603249241F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301010 5',
            mRNA sequence.
ACCESSION   BI600906
VERSION     BI600906.1  GI:15493845
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 942)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11762  row: a  column: 11
            High quality sequence stop: 762.

FEATURES             Location/Qualifiers
     source          1. .942
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5301010"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                1.85e-97      Length:          942
Score:                    1125.50       Matches:         248
Percent Similarity:       93.0%         Conservative:    6
Best Local Similarity:    90.8%         Mismatches:      13
Query Match:              75.4%         Indels:          8
DB:                       2             Gaps:            1

US-09-827-854A-2 (1-299) x BI600906 (1-942)

Qy           1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         127 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 186

Qy          21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         187 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 246

Qy          41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         247 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCAAGGAACTG 306

Qy          61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         307 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 366

Qy          81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         367 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 426

Qy         101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         427 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 486

Qy         121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         487 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 546

Qy         141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         547 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 606

Qy         161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         607 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 666

Qy         181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
               ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         667 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGC-GCCACTGTGGGCTCCCTGGCCGGC 725

Qy         201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAla-ArgMetGlu-G 220
               ||||||||||||||||||||||||||||||||||||:::|||||| ||||||||| :
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Db        726 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGGTGCGCGCCGCGGATGGAGGC 785

Qy        220 luMetGlySerArgThrArgAspArgLeuAsp-GluValLys-GluGlnValAlaGluVa 239
              :::::|||||||||||||||||||   |||||| ||||||    :::|||||||||||||||
Db        786 AGATTGGCAGCCGGACCCGCGACGGCCTGGACCGAGGTGAACGGACCAGGTTGCGGAAGT 845

Qy        239 l-ArgAlaLysLeuGluGluGlnAla---GlnGlnIleArgLeuGlnAlaGluAlaPheG 258
              | |||||||   |||||||||             :::      ||||||||||||||||   |
Db        846 TGCGCGCCAACTTGGAGGAACACGGCCCAGCAGAATACGCCTTGCAGGCCGAGGCCCTTC 905

Qy        258 lnAlaArgLeuLysSerTrpPheGluPro 267
              ||||||||||||||   |||       |||
Db        906 AGGCCCGCCTCAAAAC-TGGTTGACCCCT 933

RESULT 10
BM042676/c
LOCUS       BM042676                834 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  603616028T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420598 3',
            mRNA sequence.
ACCESSION   BM042676
VERSION     BM042676.1  GI:16771943
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1875  row: h  column: 07
            High quality sequence start: 23
            High quality sequence stop: 834.
FEATURES             Location/Qualifiers
     source          1. .834
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420598"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              2.75e-97        Length:         834
Score:                  1123.00         Matches:        241
Percent Similarity:     97.2%           Conservative:   2
Best Local Similarity:  96.4%           Mismatches:     1
Query Match:            75.2%           Indels:         6
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x BM042676 (1-834)

Qy         56 ValThrGlnGluLeuArgAlaLeuMetAspGluThrMet--LysGluLeuLysAlaTyrL 75
              |||||||||||||||||||||||||||||||||||||||  :::   ||||||||||||
Db        833 GTCACCCAGGAACTGAGGGCGCTGATGGACGAGACCATGGAAGGACGTTGAAGGCGTACA 774

Qy         75 ysSerGluLeuGlu-GluGln-LeuThrProValAlaGluGluThrArgAlaArgLeuSe 94
              |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||||
Db        773 AATCGGAACTGGAGGGAACAACCTGACCCCGGTGGCGGAGGAAACGCGGGCACGGCTGTC 714

Qy         94 rLysGlu--LeuGlnAlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGly 113
              |||:::  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 CAAGGACGCTTGCAGGCGGCGCAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGC 654

Qy        114 ArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeu 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CGCCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTG 594

Qy        134 ArgValArgLeuAlaSerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAsp 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGAT 534

Qy        154 AspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGly 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 GACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGC 474

Qy        174 LeuSerAlaIleArgGluArgLeuGlyProLeuValGluGlnGlyArgValArgAlaAla 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 CTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCC 414

Qy        194 ThrValGlySerLeuAlaGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArg 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 ACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGG 354

Qy        214 LeuArgAlaArgMetGluGluMetGlySerArgThrArgAspArgLeuAspGluValLys 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CTGCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAG 294

Qy        234 GluGlnValAlaGluValArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGln 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GAGCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAG 234

Qy        254 AlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGln 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 GCCGAGGCCTTCCAGGCCCGCCTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAG 174

Qy        274 ArgGlnTrpAlaGlyLeuValGluLysValGlnAlaAlaValGlyThrSerAlaAlaPro 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 CGCCAGTGGGCCGGGCTGGTGGAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCT 114

Qy        294 ValProSerAspAsnHis 299
              |||||||||||||||||
Db        113 GTGCCCAGCGACAATCAC 96

RESULT 11
BM042094
LOCUS       BM042094                800 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  603615713F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420618 5',
            mRNA sequence.
ACCESSION   BM042094
VERSION     BM042094.1  GI:16771361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 800)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1875  row: i  column: 03
           High quality sequence stop: 792.
FEATURES             Location/Qualifiers
     source          1. .800
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420618"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.69e-96        Length:         800
Score:                  1111.00         Matches:        226
Percent Similarity:     99.1%           Conservative:   4
Best Local Similarity:  97.4%           Mismatches:     2
Query Match:            74.4%           Indels:         1
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x BM042094 (1-800)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 163

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 223

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 283

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 343

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 403

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 463

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 523

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 583

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 643

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
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Db        644 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCAGCACTGTGGGCTCCCTGGCCGGC 703

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        704 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGTG-CGCGCGCGGATGGAGGAG 762

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluVal 232
              ||||||:::|||   |||:::|||||||||:::|||
Db        763 ATGGGCACGCGGGACCGCGAACGCCTGGACGACGTG 798

RESULT 12
BG472299
LOCUS       BG472299                927 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602513830F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645759 5',
            mRNA sequence.
ACCESSION   BG472299
VERSION     BG472299.1  GI:13404485
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1419  row: k  column: 08
            High quality sequence stop: 848.
FEATURES             Location/Qualifiers
     source          1. .927
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4645759"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_16"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.97e-96        Length:         927
Score:                  1110.50         Matches:        257
Percent Similarity:     91.8%           Conservative:   2
Best Local Similarity:  91.1%           Mismatches:     13
Query Match:            74.4%           Indels:         12
DB:                     2               Gaps:           1

US-09-827-854A-2 (1-299) x BG472299 (1-927)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 160

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 220
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Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 280

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 340

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 400

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 460

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 520

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 580

Qy        161 ValTyrGln-AlaGlyAlaArgGluGlyAlaGluArgGly--LeuSerAlaIleArgGlu 179
              |||||||| ||||||||||||||||||||||||||||||     |||||||||||||||
Db        581 GTGTACCAGGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCCTCAAGCGCCATCCGCGAG 640

Qy        180 ArgLeu--GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuA 199
              ||||||  ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        641 CGCCTTGGGGCCCCTGGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGG 700

Qy        199 laGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetG 219
              ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 CCGGCCAGCG-CTACAGGAGCGGGCCCAGGCCTGGGGCGAACGGTG-CGCGCGCGGATGG 758

Qy        219 luGluMetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu 238
              ||||||||||   ||| ||||||:::|||      ||||||||||||||||||||||||
Db        759 AGGAGATGGGGCAGCGGGACCCGCGAACGCTGGACCGAGGTGAAGGAGCAGGTGGCGGAG 818

Qy        239 -ValArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAla---Ph 257
               ||||||   ||||||||||||      ||||||||||||||||||||||||||||||||
Db        819 GGTGCGCCGCAAGCTGGAGGAAGCAGGCCAGCAGATACGGCTGCAGGCCGAGGGGCCTTC 878

Qy        257 eGlnAlaArg-LeuLysSerTrpPhe-GluProLeuValGluAspMet 272
              :::|||||| ||||||||||||||| |||||| ||||||||||||
Db        879 CAGGGCCCGGCCTCAAGAGCTGGTTCGGAGCCCTGGGTGGAAGACATG 926
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RESULT 13
BI597743
LOCUS BI597743 922 bp mRNA linear EST 07-SEP-2001
DEFINITION 603248609F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5300259 5', mRNA sequence.
ACCESSION BI597743
VERSION BI597743.1 GI:15490682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 922)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11760 row: b column: 04
High quality sequence stop: 782.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5300259"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

Pred. No.:	9.57e-96	Length:	922
Score:	1107.50	Matches:	239
Percent Similarity:	93.1%	Conservative:	4
Best Local Similarity:	91.6%	Mismatches:	14
Query Match:	74.2%	Indels:	5
DB:	2	Gaps:	1

US-09-827-854A-2 (1-299) x BI597743 (1-922)

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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 186

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 246

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 306

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 366

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 426

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 486

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 546

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        547 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 606

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        607 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCTC-AGCGCCATCCGCGAGCGC 665

Qy        181 LeuGlyProLeuVal-GluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGl 200
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Db        666 CTGGGGCCCCTGGTGGGAACAGGGCCGGGTGCCGGCCGCCACTGTGGGCTCCCTGGCCGG 725

Qy        200 yGln-ProLeuGlnGluArg-AlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGlu 219

Db        726 CCAGCCCGCTACAGGAGCGGGGCCCAGGCCTGGGGCGAGCGGATACGCGCGCGATGGACG 785

Qy        220 GluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluVal 239

Db        786 AGCAGGGGCAGCCGGACCCGAGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGGGGTG 845

Qy        240 ArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGln 258

Db        846 GGGCCACAAGCTGAAGAAACAGCCCAGAAATACGCCTTA---GCCGAAGGCTTCAGG 899
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RESULT 14
BM728696

LOCUS	BM728696 706 bp mRNA linear EST 01-MAR-2002
DEFINITION	UI-E-EJ0-aiu-l-08-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone UI-E-EJ0-aiu-l-08-0-UI 5', mRNA sequence.
ACCESSION	BM728696
VERSION	BM728696.1 GI:19050022
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 706)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PUBMED	8889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1. .706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aiu-l-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:

Pred. No.:	1.48e-95	Length:	706
Score:	1104.00	Matches:	228
Percent Similarity:	98.3%	Conservative:	0
Best Local Similarity:	98.3%	Mismatches:	2
Query Match:	73.9%	Indels:	2
DB:	3	Gaps:	0

US-09-827-854A-2 (1-299) x BM728696 (1-706)

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Qy          1 LysValGluGlnAlaVal-GluThrGluProGluProGluLeuArgGlnGlnThrGluTr 20

Db         14 AAGGTGGAGCAAGCGGTGAGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTG 73

Qy         20 pGlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArg-TrpV 40

Db         74 GCAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCGTGGG 133

Qy         40 alGlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluL 60

Db        134 TGCAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAAC 193

Qy         60 euArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluG 80

Db        194 TGAGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACACATCGGAACTGGAGG 253

Qy         80 luGlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaA 100

Db        254 AACAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGG 313

Qy        100 laGlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgG 120

Db        314 CGCAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACCGCG 373

Qy        120 lyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerH 140

Db        374 GCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCC 433

Qy        140 isLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuA 160

Db        434 ACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGG 493

Qy        160 laValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluA 180

Db        494 CAGTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGTCTCAGCGCCATCCGCGAGC 553

Qy        180 rgLeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaG 200

Db        554 GCCTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCTCTGGCCG 613

Qy        200 lyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluG 220

Db        614 GCCAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGG 673

Qy        220 luMetGlySerArgThrArgAspArgLeuAsp 230

Db        674 AGATGGGCAGCCGGACCCGCGACCGCCTGGAC 705
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RESULT 15
BF967543/c

LOCUS	BF967543 954 bp mRNA linear EST 23-JAN-2001
DEFINITION	602287404T1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4374576 3', mRNA sequence.
ACCESSION	BF967543
VERSION	BF967543.1 GI:12334758
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 954)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10038  row: h  column: 01
            High quality sequence start: 16
            High quality sequence stop: 839.
FEATURES              Location/Qualifiers
     source           1. .954
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4374576"
                      /tissue_type="hypothalamus"
                      /lab_host="DH10B"
                      /clone_lib="NIH_MGC_96"
                      /note="Organ: brain; Vector: pBluescriptR (modified
                      pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                      (gtcgag); Oligo-dT primed using primer
                      5'-TTTTTTTTTTTTTTTTVN-3', size-selected for  average
                      insert size 2.3 kb and normalized to ROT 5. This is a
                      primary library enriched for full-length  clones and
                      constructed using the Cap-trapper method (Carninci, in
                      preparation).  Library constructed by M. Brownstein
                      (NIMH/NHGRI, National Institutes of Health). Note: this is
                      a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              6.53e-95        Length:         954
Score:                  1099.00         Matches:        243
Percent Similarity:     95.4%           Conservative:   4
Best Local Similarity:  93.8%           Mismatches:     6
Query Match:            73.6%           Indels:         7
DB:                     2               Gaps:           0

US-09-827-854A-2 (1-299) x BF967543 (1-954)

Qy         47 ValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu-ArgAla-LeuMetAspG 66
              |||||||||||||||   ||||||:::|||||||||||||||| |||||| ||||||||||
Db        883 GTCCAGGAGGAGCTGTTCAGCTCCAGAGTCACCCAGGAACTGGAGGGCGCTTGATGGACG 824

Qy         66 luThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu-GlnLeuThrProVal 85
              ||||||||||||||||||            :::|||||||||| ||||||||||||||||
Db        823 AGACCATGAAGGAGTTGAAGCCTACAAATCGGAAACTGGAGGAACCAACTGACCCCGGTG 764

Qy         86 AlaGluGluThr-ArgAlaArgLeuSer--LysGluLeuGlnAlaAlaGlnAlaArgLeu 104
              |||||||||||| ||||||||||||||  :::|||||||||||||||||||||||||||
Db        763 GCGGAGGAGACGGCGGGCACGGCTGTCCCAAGGGAGCTGCAGGCGGCGCAGGCCCGGCTG 704

Qy        105 GlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGlnAla 124
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Db        703 GGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGCGAGGTGCAGGCC 644

Qy        125 MetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLysLeu 144
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Db        643 ATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTG 584

Qy        145 ArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGlnAla 164
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Db        583 CGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCC 524

Qy        165 GlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyProLeu 184
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Db        523 GGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTG 464

Qy        185 ValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeuGln 204
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Db        463 GTGGAACGGGGCCGCGTGCGGGCCGCCACTGTGGGCTC-CTGGCCGGCCAGCCGCTACAG 405

Qy        205 GluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySerArg 224
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Db        404 GAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGATGGGCAGCCGG 345

Qy        225 ThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeuGlu 244
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Db        344 ACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAGCTGGAG 285

Qy        245 GluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSerTrp 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCTGG 225

Qy        265 PheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysValGln 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 TTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTGGAGAAGGTGCAG 165

Qy        285 AlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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Search completed: June 15, 2006, 00:06:14
Job time : 7925.48 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:03:31 ; Search time 312.205 Seconds
(without alignments)
2687.952 Million cell updates/sec

Title: US-09-827-854A-2
Perfect score: 1493
Sequence: 1 KVEQAVETEPEPELRQQTEW.....VEKVQAAVGTSAAPVPSDNH 299

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
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-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1493	100.0	1156	3	US-09-023-655-1007	Sequence 1007, Ap
2	1493	100.0	1291	3	US-09-919-039-246	Sequence 246, App
3	1484	99.4	1157	2	US-07-709-949-1	Sequence 1, Appli
4	1484	99.4	1157	4	US-09-880-107-2244	Sequence 2244, Ap
5	1363.5	91.3	3805	3	US-09-108-006C-3	Sequence 3, Appli
6	1082	72.5	1126	3	US-08-949-155-5	Sequence 5, Appli
7	1082	72.5	1126	3	US-09-819-964-5	Sequence 5, Appli
8	1026	68.7	664	4	US-10-211-689-37	Sequence 37, Appl
9	1026	68.7	718	4	US-10-211-689-35	Sequence 35, Appl
10	1026	68.7	802	4	US-10-211-689-31	Sequence 31, Appl
11	997	66.8	652	4	US-10-211-689-43	Sequence 43, Appl
12	997	66.8	709	4	US-10-211-689-41	Sequence 41, Appl
13	997	66.8	788	4	US-10-211-689-33	Sequence 33, Appl
14	992	66.4	4267	3	US-08-949-155-51	Sequence 51, Appl
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16	973	65.2	691	4	US-10-211-689-45	Sequence 45, Appl
17	892	59.7	660	2	US-08-726-306A-28	Sequence 28, Appl
18	855	57.3	616	4	US-10-211-689-39	Sequence 39, Appl
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c 20	533	35.7	478	4	US-09-880-107-2491	Sequence 2491, Ap
21	511	34.2	330	2	US-07-849-389-6	Sequence 6, Appli
22	412	27.6	405	3	US-09-513-999C-2137	Sequence 2137, Ap
23	374	25.1	252	3	US-08-617-256-24	Sequence 24, Appl
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25	374	25.1	252	3	US-09-431-613-24	Sequence 24, Appl
26	374	25.1	252	3	US-09-504-245-24	Sequence 24, Appl
27	374	25.1	252	3	US-09-287-682-24	Sequence 24, Appl
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32	374	25.1	252	3	US-09-796-416-24	Sequence 24, Appl
33	374	25.1	252	3	US-09-879-341-24	Sequence 24, Appl
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37	258.5	17.3	1469	3	US-09-949-016-4983	Sequence 4983, Ap
38	224	15.0	121	3	US-09-818-875-3400	Sequence 3400, Ap
c 39	224	15.0	121	3	US-09-818-875-3401	Sequence 3401, Ap
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c 41	219	14.7	121	3	US-09-818-875-3405	Sequence 3405, Ap
42	210	14.1	7065	3	US-09-874-923-115	Sequence 115, App
43	205.5	13.8	6604	3	US-09-949-016-16725	Sequence 16725, A
44	198	13.3	121	3	US-09-818-875-3464	Sequence 3464, Ap
c 45	198	13.3	121	3	US-09-818-875-3465	Sequence 3465, Ap

ALIGNMENTS

RESULT 1
US-09-023-655-1007
; Sequence 1007, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1007:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1156 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g178850
US-09-023-655-1007

Alignment Scores:
Pred. No.:                3.86e-135       Length:         1156
Score:                    1493.00         Matches:        299
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-09-827-854A-2 (1-299) x US-09-023-655-1007 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 2
US-09-919-039-246
; Sequence 246, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 246
;   LENGTH: 1291
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 2514988CB1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 46
;   OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-246

Alignment Scores:
Pred. No.:                4.47e-135       Length:         1291
Score:                    1493.00         Matches:        299
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-09-827-854A-2 (1-299) x US-09-919-039-246 (1-1291)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 299

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 359

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 419

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 479

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 539

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        540 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 599

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 659

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 719

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 779

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 839

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 899

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 959

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 1019

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 1079

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1136

RESULT 3
US-07-709-949-1
; Sequence 1, Application US/07709949
; Patent No. 5472858
;  GENERAL INFORMATION:
;    APPLICANT:  Attie, Alan D
;    APPLICANT:  Gretch, Daniel G
;    APPLICANT:  Sturley, Stephen L
;    APPLICANT:  Beckage, Nancy E
;    TITLE OF INVENTION:  Production of Recombinant Proteins in
;    TITLE OF INVENTION:  Insect Larvae
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  P.O. Box 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/709,949
;      FILING DATE:  19910604
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  9629691801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 251-5000
;      TELEFAX:  (608)251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1157 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  62..1015
;    FEATURE:
;      NAME/KEY:  misc_signal
;      LOCATION:  62..119
;    PUBLICATION INFORMATION:
;      AUTHORS:  McLean, J W
;      JOURNAL:  Journal of Biological Chemistry
;      VOLUME:  259
;      PAGES:  6498-6504
;      DATE:  1984
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 1157
US-07-709-949-1

Alignment Scores:
Pred. No.:                2.86e-134       Length:          1157
Score:                    1484.00         Matches:         297
Percent Similarity:       99.3%           Conservative:    0
Best Local Similarity:    99.3%           Mismatches:      2
Query Match:              99.4%           Indels:          0
DB:                       2               Gaps:            0

US-09-827-854A-2 (1-299) x US-07-709-949-1 (1-1157)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 175

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 235

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAAGTCACCCAAGAACTG 295

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 355

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        356 CAACTGACCCCGGTAGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGACGGCG 415

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 475

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 535

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        536 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATCCCGATGACCTGCAGAAGCGCCTGGCA 595

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 655
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Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 715

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 775

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 ATGGGCAGTCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 835

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 895

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 955

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1012

RESULT 4
US-09-880-107-2244
; Sequence 2244, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. 6974667 M12529
US-09-880-107-2244

Alignment Scores:
Pred. No.:              2.86e-134       Length:         1157
Score:                  1484.00         Matches:        297
Percent Similarity:     99.3%           Conservative:   0
Best Local Similarity:  99.3%           Mismatches:     2
Query Match:            99.4%           Indels:         0
DB:                     4               Gaps:           0

US-09-827-854A-2 (1-299) x US-09-880-107-2244 (1-1157)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 175

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 235

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAAGTCACCCAAGAACTG 295

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 355

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 CAACTGACCCCGGTAGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGACGGCG 415

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 475

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 535

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATCCCGATGACCTGCAGAAGCGCCTGGCA 595

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 655

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 715

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 775

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 ATGGGCAGTCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 835

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 895

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 955

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1012

RESULT 5
US-09-108-006C-3
; Sequence 3, Application US/09108006C
; Patent No. 6524613
;  GENERAL INFORMATION:
;       APPLICANT: Steer, Clifford J.
;                  Kren, Betsy T.
;                  Bandyopadhyay, Paramita
;                  Roy-Chowdhury, Jayanta
;       TITLE OF INVENTION: Hepatocellular Chimeraplasty
;       NUMBER OF SEQUENCES: 62
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Kimeragen, Inc.
;            STREET: 300 Pheasant Run
;            CITY: Newtown
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 18940
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/108,006C
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;             FILING DATE: 30-Jun-1992
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/054,288
;             FILING DATE: 30-APR-1997
;             APPLICATION NUMBER: 60/054,837
;             FILING DATE: 05-AUG-1997
;             APPLICATION NUMBER: 60/064,996
;             FILING DATE: 10-NOV-1997
;             APPLICATION NUMBER: 60/074,497
;             FILING DATE: 12-FEB-1998
;             APPLICATION NUMBER: PCT US 98/08834
;             FILING DATE: 30-APR-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Friebel, Thomas
;             REGISTRATION NUMBER: 29258
;             REFERENCE/DOCKET NUMBER: 7991-015-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-504-4444
;             TELEFAX: 215-504-4545
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3805 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Genomic DNA
;        FEATURE:
;             NAME/KEY:  exon
;             LOCATION:  71...114
;             OTHER INFORMATION:  Exon 1
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-108-006C-3

Alignment Scores:
Pred. No.:              6.27e-122       Length:         3805
Score:                  1363.50         Matches:        298
Percent Similarity:     60.4%           Conservative:   0
Best Local Similarity:  60.4%           Mismatches:     1
Query Match:            91.3%           Indels:         195
DB:                     3               Gaps:           1

US-09-827-854A-2 (1-299) x US-09-108-006C-3 (1-3805)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 2101

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 2161

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACT- 2220

Qy         60 ------------------------------------------------------------ 60

Db       2221 GAGGTGAGTGTCCCCATCCTGGCCCTTGACCCTCCTGGTGGGCGGCTATACCTCCCCAGG 2280

Qy         60 ------------------------------------------------------------ 60

Db       2281 TCCAGGTTTCATTCTGCCCCTGTCGCTAAGTCTTGGGGGGCCTGGGTCTCTGCTGGTTCT 2340

Qy         60 ------------------------------------------------------------ 60

Db       2341 AGCTTCCTCTTCCCATTTCTGACTCCTGGCTTTAGCTCTCTGGAATTCTCTCTCTCAGCT 2400

Qy         60 ------------------------------------------------------------ 60

Db       2401 TTGTCTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCCTGGCTCTGTCTCTGT 2460

Qy         60 ------------------------------------------------------------ 60

Db       2461 CCTTCCCTAGCTCTTTTATATAGAGACAGAGAGATGGGGTCTCACTGTGTTGCCCAGGCT 2520

Qy         60 ------------------------------------------------------------ 60

Db       2521 GGTCTTGAACTTCTGGGCTCAAGCGATCCTCCCGCCTCGGCCTCCCAAAGTGCTGGGATT 2580

Qy         60 ------------------------------------------------------------ 60

Db       2581 AGAGGCATGAGCACCTTGCCCGGCCTCCTAGCTCCTTCTTCGTCTCTGCCTCTGCCCTCT 2640

Qy         60 ------------------------------------------------------------ 60

Db       2641 GCATCTGCTCTCTGCATCTGTCTCTGTCTCCTTCTCTCGGCCTCTGCCCCGTTCCTTCTC 2700

Qy         60 ------------------------------------------------------------ 60

Db       2701 TCCCTCTTGGGTCTCTCTGGCTCATCCCCATCTCGCCCGCCCCATCCCAGCCCTTCTCCC 2760

Qy         61 ----------------------------------------ArgAlaLeuMetAspGlu 66
                                                      ||||||||||||||||||
Db       2761 CCGCCTCCCCACTGTGCGACACCCTCCCGCCCTCTCGGCCGCAGGGCGCTGATGGACGAG 2820

Qy         67 ThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGluGlnLeuThrProValAla 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 ACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAACAACTGACCCCGGTGGCG 2880

Qy         87 GluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArgLeuGlyAla 106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGGGCGCG 2940

Qy        107 AspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeu 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTC 3000

Qy        127 GlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLysLeuArgLys 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAG 3060

Qy        147 ArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAla 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGGCC 3120

Qy        167 ArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyProLeuValGlu 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTGGTGGAA 3180

Qy        187 GlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeuGlnGluArg 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGG 3240

Qy        207 AlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySerArgThrArg 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGC 3300

Qy        227 AspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeuGluGluGln 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAG 3360

Qy        247 AlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGlu 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCTGGTTCGAG 3420

Qy        267 ProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysValGlnAlaAla 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 CCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTGGAGAAGGTGCAGGCTGCC 3480

Qy        287 ValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              ||||||||||||||||||||||||||||||||||||||
Db       3481 GTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 3519

RESULT 6
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US-08-949-155-5
; Sequence 5, Application US/08949155
; Patent No. 6271436
;  GENERAL INFORMATION:
;    APPLICANT:  Piedrahita, Jorge A
;    APPLICANT:  Bazer, Fuller W
;    TITLE OF INVENTION:  Compositions and Methods for the
;    TITLE OF INVENTION:  Generation of Transgenic Animal Species
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE AND DURKEE
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/949,155
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/027,338
;      FILING DATE:  11-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/046,094
;      FILING DATE:  09-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hibler, David W.
;      REGISTRATION NUMBER:  41,071
;      REFERENCE/DOCKET NUMBER:  TAMK:177
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1126 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  51..1001
US-08-949-155-5

Alignment Scores:
Pred. No.:              2.04e-95        Length:         1126
Score:                  1082.00         Matches:        212
Percent Similarity:     85.1%           Conservative:   40
Best Local Similarity:  71.6%           Mismatches:     40
Query Match:            72.5%           Indels:         4
DB:                     3               Gaps:           2

US-09-827-854A-2 (1-299) x US-08-949-155-5 (1-1126)

Qy          7 GluThrGluProGluProGluLeuArg---------GlnGlnThrGluTrpGlnSerGly 23
              |||      |||   ||||||:::           ::::::   :::||||||
Db        111 GAGCCGGGGCCGCCGCCGGAGGTGCACGTGTGGTGGGAGGAGCCCAAGTGGCAGGGCAGC 170

Qy         24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        171 CAGCCCTGGGAGCAGGCCCTGGGCCGCTTCTGGGATTACCTGCGCTGGGTGCAGTCCCTG 230

Qy         44 SerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeuArgAlaLeu 63
              |||:::|||||||||||||||||||||||||:::::|||||||||||||||      |||
Db        231 TCTGACCAAGTGCAGGAGGAGCTGCTCAGCACCAAGGTCACCCAGGAACTGACGGAGCTG 290

Qy         64 MetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGluGlnLeuThr 83
              ::::::|||:::||||||||||:::||||||||:::   |||||||||   ||||||

Db        291 ATAGAGGAGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTGGAGGCGCAGCTGGGC 350

Qy         84 ProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArg 103
              ||||||   :::||||||:::||||||||||||||||||||||||||||||||||||||
Db        351 CCCGTGACCCAGGAGACGCAGGCGCGCCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGC 410

Qy        104 LeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
              :::|||||||||||||||||||||||      ||||||||   ||||||   ||||||
Db        411 GTGGGCGCCGACATGGAGGACGTGCGCAACCGCTTGGTGCTCTACCGCAGCGAGGTGCAC 470

Qy        124 AlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLys 143
              ||||||||||||:::|||||||||||||||   ||||||||||||||||||||||||||
Db        471 AACATGTTGGGCCAGACCACCGAGGAGCTGCGGAGCCGCCTGGCTTCCCACCTGCGCAAG 530

Qy        144 LeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGln 163
              ||||||||||||||||||||||   :::|||||||||||||||||||||||||||||||
Db        531 CTGCGCAAGCGGCTGCTCCGCGACACCGAGGACCTGCAGAAGCGCCTGGCCGTGTACCAG 590

Qy        164 AlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyPro 183
              ||||||   ||||||||||||||||||   :::|||||:::||||||||||||||||||
Db        591 GCGGGGCTGCGCGAGGGCGCCGAGCGCAGCGTGAGCGCCCTCCGCGAGCGCCTCGGGCCC 650

Qy        184 LeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeu 203
              ||||||||||||||||||:::||||||||||||:::   :::   ||||||||||||||||
Db        651 CTGGTGGAGCAGGGCCGATTGCGCGCCGCCACCCTGAGTACCAGGGCCGGCCAGCCGCTG 710

Qy        204 GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer 223
              :::||||||||:::||||||||:::::|||||   |||:::|||||||||||||||||
Db        711 CGCGAGCGCGCGGAAGCCTGGGGCCAGAAGCTGCGCGGACGGCTGGAGGAGATGGGCAGC 770

Qy        224 ArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeu 243
              ||||||||||||||||||||||:::::|||||:::   |||||||||   |||:::
Db        771 CGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAGGTGCGCACCAAAGTG 830

Qy        244 GluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer 263
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Db        831 GAGGAGCAGGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCACGCCCTCCTCAAAGGC 890

Qy        264 TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal 283
              ||||||||||||||||||||||:::::|||||||||||||||||||||||||:::::
Db        891 TGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCGGGCTGGTGGAGAGGATG 950

Qy        284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
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Db        951 CAGTCGGCCGTGAGCATAAGCTCCTCCACCTCTGCGCCCAGTGATAAT 998

RESULT 7
US-09-819-964-5
; Sequence 5, Application US/09819964
; Patent No. 6369294
;  GENERAL INFORMATION:
;       APPLICANT: Piedrahita, Jorge A
;                  Bazer, Fuller W
;       TITLE OF INVENTION: Compositions and Methods for the
;                           Generation of Transgenic Animal Species
;       NUMBER OF SEQUENCES: 51
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: ARNOLD, WHITE AND DURKEE
;            STREET: P.O. Box 4433
;            CITY: Houston
;            STATE: TX
;            COUNTRY: US
;            ZIP: 77210-4433
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/819,964
;            FILING DATE: 28-Mar-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: 08/949,155
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 60/046,094
;             FILING DATE: 09-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Hibler, David W.
;             REGISTRATION NUMBER: 41,071
;             REFERENCE/DOCKET NUMBER: TAMK:177
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (512) 418-3000
;             TELEFAX: (713) 789-2679
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1126 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  51..1001
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-819-964-5

Alignment Scores:
Pred. No.:              2.04e-95      Length:         1126
Score:                  1082.00       Matches:        212
Percent Similarity:     85.1%         Conservative:   40
Best Local Similarity:  71.6%         Mismatches:     40
Query Match:            72.5%         Indels:         4
DB:                     3             Gaps:           2

US-09-827-854A-2 (1-299) x US-09-819-964-5 (1-1126)

Qy          7 GluThrGluProGluProGluLeuArg---------GlnGlnThrGluTrpGlnSerGly 23
              |||       |||   ||||||:::           ::::::   :::|||||||
Db        111 GAGCCGGGGCCGCCGCCGGAGGTGCACGTGTGGTGGGAGGAGCCCAAGTGGCAGGGCAGC 170

Qy         24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43
              |||   ||||||   ||||||||||||||||||||||||||||||||||||:::|||
Db        171 CAGCCCTGGGAGCAGGCCCTGGGCCGCTTCTGGGATTACCTGCGCTGGGTGCAGTCCCTG 230

Qy         44 SerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeuArgAlaLeu 63
              |||:::|||||||||||||||||||||||:::::::|||||||||||||||||      |||
Db        231 TCTGACCAAGTGCAGGAGGAGCTGCTCAGCACCAAGGTCACCCAGGAACTGACGGAGCTG 290

Qy         64 MetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGluGlnLeuThr 83
              ::::::|||:::|||||||||:::|||||||||::   |||||||||   ||||||
Db        291 ATAGAGGAGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTGGAGGCGCAGCTGGGC 350

Qy         84 ProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArg 103
              ||||||   :::||||||:::||||||||||||||||||||||||||||||||||||||
Db        351 CCCGTGACCCAGGAGACGCAGGCGCGCCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGC 410

Qy        104 LeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
              :::|||||||||||||||||||      ||||||||   ||||||  ||||||
Db        411 GTGGGCGCCGACATGGAGGACGTGCGCAACCGCTTGGTGCTCTACCGCAGCGAGGTGCAC 470

Qy        124 AlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLys 143
                 ||||||||||:::|||||||||||||   ||||||||||||||||||||||
Db        471 AACATGTTGGGCCAGACCACCGAGGAGCTGCGGAGCCGCCTGGCTTCCCACCTGCGCAAG 530

Qy        144 LeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGln 163
              ||||||||||||||||||||    :::||||||||||||||||||||||||||||||
Db        531 CTGCGCAAGCGGCTGCTCCGCGACACCGAGGACCTGCAGAAGCGCCTGGCCGTGTACCAG 590

Qy        164 AlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyPro 183
              ||||||   ||||||||||||||||||   :::|||||:::||||||||||||||||||
Db        591 GCGGGGCTGCGCGAGGGCGCCGAGCGCAGCGTGAGCGCCCTCCGCGAGCGCCTCGGGCCC 650

Qy        184 LeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeu 203
              ||||||||||||||||||:::|||||||||||:::   :::   ||||||||||||||
Db        651 CTGGTGGAGCAGGGCCGATTGCGCGCCGCCACCCTGAGTACCAGGGCCGGCCAGCCGCTG 710

Qy        204 GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer 223
              :::||||||||:::||||||||:::::|||||   |||:::||||||||||||||||
Db        711 CGCGAGCGCGCGGAAGCCTGGGGCCAGAAGCTGCGCGGACGGCTGGAGGAGATGGGCAGC 770

Qy        224 ArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeu 243
              ||||||||||||||||||||||||:::::|||||:::   ||||||||   |||:::
Db        771 CGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAGGTGCGCACCAAAGTG 830

Qy        244 GluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer 263
              |||||||||      |||:::|||||||||||||||   |||   |||   ||||||
Db        831 GAGGAGCAGGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCACGCCCTCCTCAAAGGC 890

Qy        264 TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal 283
              ||||||||||||||||||||||||:::::|||||||||||||||||||||||:::::
Db        891 TGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCGGGCTGGTGGAGAGGATG 950

Qy        284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
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Db        951 CAGTCGGCCGTGAGCATAAGCTCCTCCACCTCTGCGCCCAGTGATAAT 998

RESULT 8
US-10-211-689-37
; Sequence 37, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
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;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 37
;   LENGTH: 664
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(664)
US-10-211-689-37

Alignment Scores:
Pred. No.:              2.62e-90        Length:         664
Score:                  1026.00         Matches:        214
Percent Similarity:     71.6%           Conservative:   0
Best Local Similarity:  71.6%           Mismatches:     1
Query Match:            68.7%           Indels:         84
DB:                     4               Gaps:           1

US-09-827-854A-2 (1-299) x US-10-211-689-37 (1-664)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db         11 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 70

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 130

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 190

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 250

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAG---------- 298

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db        298 ------------------------------------------------------------ 298

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db        298 ------------------------------------------------------------ 298

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160

Db        298 ------------------------------------------------------------ 298

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        298 ------------------------------------------------------------ 298

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db        299 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTTCCTGGCCGGC 358

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 418

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 478

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 538

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 598

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 655

RESULT 9
US-10-211-689-35
; Sequence 35, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
;   LENGTH: 718
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(718)
US-10-211-689-35

Alignment Scores:
Pred. No.:              2.91e-90        Length:         718
Score:                  1026.00         Matches:        214
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Percent Similarity:     71.6%          Conservative:  0
Best Local Similarity:  71.6%          Mismatches:    1
Query Match:            68.7%          Indels:        84
DB:                     4              Gaps:          1

US-09-827-854A-2 (1-299) x US-10-211-689-35 (1-718)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 124

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 184

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 244

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 304

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAG---------- 352

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db        352 ---------------------------------------------------------- 352

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db        352 ---------------------------------------------------------- 352

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160

Db        352 ---------------------------------------------------------- 352

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        352 ---------------------------------------------------------- 352

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db        353 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTTCCTGGCCGGC 412

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 472

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 532

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 592

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 652

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 709

RESULT 10
US-10-211-689-31
; Sequence 31, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT: Anderson, David W.
;  APPLICANT: Boldog, Ferenc L.
;  APPLICANT: Burgess, Catherine E.
;  APPLICANT: Casman, Stacie J.
;  APPLICANT: Edinger, Shlomit R.
;  APPLICANT: Gangolli, Esha A.
;  APPLICANT: Gorman, Linda
;  APPLICANT: Guo, Xiaojia (Sasha)
;  APPLICANT: Khramstov, Nikolai V.
;  APPLICANT: Lepley, Denise M.
;  APPLICANT: MacDougall, John R.
;  APPLICANT: Pena, Carol A.
;  APPLICANT: Peyman, John A.
;  APPLICANT: Patturajan, Meera
;  APPLICANT: Rieger, Daniel K.
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT: Smithson, Glennda
;  APPLICANT: Spytek, Kimberly A.
;  APPLICANT: Vernet, Corine A. M.
;  APPLICANT: Voss, Edward Z.
;  APPLICANT: Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 31
;   LENGTH: 802
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(716)
US-10-211-689-31

Alignment Scores:
Pred. No.:              3.37e-90       Length:        802
Score:                  1026.00        Matches:       214
Percent Similarity:     71.6%          Conservative:  0
Best Local Similarity:  71.6%          Mismatches:    1
Query Match:            68.7%          Indels:        84
DB:                     4              Gaps:          1

US-09-827-854A-2 (1-299) x US-10-211-689-31 (1-802)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 131

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        132 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 191

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 251

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 311

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAG---------- 359

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db        359 ------------------------------------------------------------ 359

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db        359 ------------------------------------------------------------ 359

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160

Db        359 ------------------------------------------------------------ 359

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        359 ------------------------------------------------------------ 359

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        360 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTTCCTGGCCGGC 419

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 479

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 539

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 599

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 659

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 716

RESULT 11
US-10-211-689-43
; Sequence 43, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 43
;   LENGTH: 652
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(652)
US-10-211-689-43

Alignment Scores:
Pred. No.:                1.63e-87        Length:         652
Score:                    997.00          Matches:        210
Percent Similarity:       70.2%           Conservative:   0
Best Local Similarity:    70.2%           Mismatches:     1
Query Match:              66.8%           Indels:         88
DB:                       4               Gaps:           1

US-09-827-854A-2 (1-299) x US-10-211-689-43 (1-652)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 70

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 130

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 190

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 250

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 310
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        311 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACCGCGGC 370

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 430

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||
Db        431 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGAC------------------ 472

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        472 ------------------------------------------------------------ 472

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

Db        472 ------------------------------------------------------------ 472

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220

Db        472 ------------------------------------------------------------ 472

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240

Db        472 ------------------------------------------------------------ 472

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ------CTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 526

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 586

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 643
```

```
RESULT 12
US-10-211-689-41
; Sequence 41, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 41
;   LENGTH: 709
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(709)
US-10-211-689-41

Alignment Scores:
Pred. No.:              1.82e-87        Length:         709
Score:                  997.00          Matches:        210
Percent Similarity:     70.2%           Conservative:   0
Best Local Similarity:  70.2%           Mismatches:     1
Query Match:            66.8%           Indels:         88
DB:                     4               Gaps:           1

US-09-827-854A-2 (1-299) x US-10-211-689-41 (1-709)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 127

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 187

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 247

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 307

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 367

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        368 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACCGCGGC 427

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 487

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||
Db        488 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGAC------------------ 529
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Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        529 ------------------------------------------------------------ 529

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

Db        529 ------------------------------------------------------------ 529

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220

Db        529 ------------------------------------------------------------ 529

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240

Db        529 ------------------------------------------------------------ 529

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 ------CTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 583

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 643

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 700

RESULT 13
US-10-211-689-33
; Sequence 33, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 33
;   LENGTH: 788
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(704)
US-10-211-689-33

Alignment Scores:
Pred. No.:                2.1e-87        Length:          788
Score:                    997.00         Matches:         210
Percent Similarity:       70.2%          Conservative:    0
Best Local Similarity:    70.2%          Mismatches:      1
Query Match:              66.8%          Indels:          88
DB:                       4              Gaps:            1

US-09-827-854A-2 (1-299) x US-10-211-689-33 (1-788)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 131

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 191

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 251

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 311

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 371

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        372 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACCGCGGC 431

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 491

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||
Db        492 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGAC---------------------- 533

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180

Db        533 ------------------------------------------------------------ 533

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

Db        533 ------------------------------------------------------------ 533

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220

Db        533 ------------------------------------------------------------ 533

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        533 ------------------------------------------------------------ 533

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 ------CTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 587

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 647

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 704

RESULT 14
US-08-949-155-51
; Sequence 51, Application US/08949155
; Patent No. 6271436
;  GENERAL INFORMATION:
;    APPLICANT:  Piedrahita, Jorge A
;    APPLICANT:  Bazer, Fuller W
;    TITLE OF INVENTION:  Compositions and Methods for the
;    TITLE OF INVENTION:  Generation of Transgenic Animal Species
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE AND DURKEE
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/949,155
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/027,338
;      FILING DATE:  11-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/046,094
;      FILING DATE:  09-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hibler, David W.
;      REGISTRATION NUMBER:  41,071
;      REFERENCE/DOCKET NUMBER:  TAMK:177
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4267 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-949-155-51

Alignment Scores:
Pred. No.:              6.07e-86      Length:          4267
Score:                  992.00        Matches:         212
Percent Similarity:     59.9%         Conservative:    40
Best Local Similarity:  50.4%         Mismatches:      40
Query Match:            66.4%         Indels:          130
DB:                     3             Gaps:            3

US-09-827-854A-2 (1-299) x US-08-949-155-51 (1-4267)

Qy          7 GluThrGluProGluProGluLeuArg---------GlnGlnThrGluTrpGlnSerGly 23
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              |||      |||   ||||||:::            ::::::   :::||||||
Db       2490 GAGCCGGGGCCGCCGCCGGAGGTGCACGTGTGGTGGGAGGAGCCCAAGTGGCAGGGCAGC 2549

Qy         24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43
              |||   ||||||   ||||||||||||||||||||||||||||||||||||:::|||
Db       2550 CAGCCCTGGGAGCAGGCCCTGGGCCGCTTCTGGGATTACCTGCGCTGGGTGCAGTCCCTG 2609

Qy         44 SerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu--------- 60
              |||:::|||||||||||||||||||||||||:::::|||||||||||
Db       2610 TCTGACCAAGTGCAGGAGGAGCTGCTCAGCACCAAGGTCACCCAGGAACT-GACGTAAGT 2668

Qy         60 ------------------------------------------------------------ 60

Db       2669 GCCCACCCGACTCCCGCCGCGCGCGCGCGCGCGCGCGCGCGCCTGACCCTCCTGGCGA 2728

Qy         60 ------------------------------------------------------------ 60

Db       2729 ACCGTGTGTTCTGGACCCTCAGGCTCCACCCGTCCGGGTTTCCTTCTGTCCTTGTCGCCA 2788

Qy         60 ------------------------------------------------------------ 60

Db       2789 ACTCTTGGGGGTCTGGGTCTCTGTTTCTTTTTTTCCTTCCTCCTTTTTGGGGGGAAAA 2848

Qy         60 ------------------------------------------------------------ 60

Db       2849 AACTTTTTCTTTTTTCTTTCATTTGACTTCATGTCTTGCTTTCTTTCCATCTTGAGCTCC 2908

Qy         60 ------------------------------------------------------------ 60

Db       2909 TGCCTTCGCCTGTCTCTGGGTCAGTCTTGCCGTCCCTTGCTGTCTCTGAATCTCTGGCAC 2968

Qy         60 ------------------------------------------------------------ 60

Db       2969 GTCCTGGCCATCGCCAGCTCAGGAGCCCTCCTTCTCCCCCTCACCGCCCCCGCCCTCTCT 3028

Qy         61 ------ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeu 78
                    |||   |||::::::|||:::|||||||||:::|||||||||:::   ||||||
Db       3029 GCGCCCAGGGAGCTGATAGAGGAGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTG 3088

Qy         79 GluGluGlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGln 98
              |||   ||||||   ||||||   :::|||||||:::|||||||||||||||||||||||
Db       3089 GAGGCGCAGCTGGGCCCCGTGACCCAGGAGACGCAGGCGCGCCTGTCCAAGGAGCTGCAG 3148

Qy         99 AlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyr 118
              ||||||||||||||:::|||||||||||||||||||      ||||||||   |||
Db       3149 GCGGCGCAGGCCCGCGTGGGCGCCGACATGGAGGACGTGCGCAACCGCTTGGTGCTCTAC 3208

Qy        119 ArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAla 138
              |||   ||||||      ||||||||||||:::|||||||||||||||   ||||||||
Db       3209 CGCAGCGAGGTGCACAACATGTTGGGCCAGACCACCGAGGAGCTGCGGAGCCGCCTGGCT 3268

Qy        139 SerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArg 158
              |||||||||||||||||||||||||||||||||||||||||||   :::|||||||||||||
Db       3269 TCCCACCTGCGCAAGCTGCGCAAGCGGCTGCTCCGCGACACCGAGGACCTGCAGAAGCGC 3328

Qy        159 LeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArg 178
              |||||||||||||||||||   |||||||||||||||||||   :::||||||:::|||
Db       3329 CTGGCCGTGTACCAGGCGGGGCTGCGCGAGGGCGCCGAGCGCAGCGTGAGCGCCCTCCGC 3388

Qy        179 GluArgLeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeu 198
              |||||||||||||||||||||||||||||||:::|||||||||||:::   :::
Db       3389 GAGCGCCTCGGGCCCCTGGTGGAGCAGGGCCGATTGCGCGCCGCCACCCTGAGTACCAGG 3448

Qy        199 AlaGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMet 218
              ||||||||||||||:::|||||||||:::|||||||||:::::::||||||   |||:::
Db       3449 GCCGGCCAGCCGCTGCGCGAGCGCGCGGAAGCCTGGGGCCAGAAGCTGCGCGGACGGCTG 3508

Qy        219 GluGluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu 238
              |||||||||||||||||||||||||||||||||||:::::||||||:::   |||
Db       3509 GAGGAGATGGGCAGCCGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAG 3568

Qy        239 ValArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGln 258
              ||||||   |||:::|||||||||      |||:::|||||||||||||||   |||
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Db       3569 GTGCGCACCAAAGTGGAGGAGCAGGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCAC 3628

Qy        259 AlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGly 278

Db       3629 GCCCTCCTCAAAGGCTGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCGGG 3688

Qy        279 LeuValGluLysValGlnAlaAlaValGly---ThrSerAlaAlaProValProSerAsp 297

Db       3689 CTGGTGGAGAGGATGCAGTCGGCCGTGAGCATAAGCTCCTCCACCTCTGCGCCCAGTGAT 3748

Qy        298 Asn 298

Db       3749 AAT 3751

RESULT 15
US-09-819-964-51
; Sequence 51, Application US/09819964
; Patent No. 6369294
;   GENERAL INFORMATION:
;        APPLICANT: Piedrahita, Jorge A
;                   Bazer, Fuller W
;        TITLE OF INVENTION: Compositions and Methods for the
;                            Generation of Transgenic Animal Species
;        NUMBER OF SEQUENCES: 51
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ARNOLD, WHITE AND DURKEE
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: TX
;             COUNTRY: US
;             ZIP: 77210-4433
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/819,964
;             FILING DATE: 28-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/949,155
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 60/046,094
;             FILING DATE: 09-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hibler, David W.
;             REGISTRATION NUMBER: 41,071
;             REFERENCE/DOCKET NUMBER: TAMK:177
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (512) 418-3000
;             TELEFAX: (713) 789-2679
;   INFORMATION FOR SEQ ID NO: 51:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4267 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-819-964-51

Alignment Scores:
Pred. No.:                6.07e-86        Length:          4267
Score:                    992.00          Matches:         212
Percent Similarity:       59.9%           Conservative:    40
Best Local Similarity:    50.4%           Mismatches:      40
Query Match:              66.4%           Indels:          130
DB:                       3               Gaps:            3

US-09-827-854A-2 (1-299) x US-09-819-964-51 (1-4267)

Qy          7 GluThrGluProGluProGluLeuArg---------GlnGlnThrGluTrpGlnSerGly 23

Db       2490 GAGCCGGGGCCGCCGCCGGAGGTGCACGTGTGGTGGGAGGAGCCCAAGTGGCAGGGCAGC 2549

Qy         24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43

Db       2550 CAGCCCTGGGAGCAGGCCCTGGGCCGCTTCTGGGATTACCTGCGCTGGGTGCAGTCCCTG 2609

Qy         44 SerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu--------- 60

Db       2610 TCTGACCAAGTGCAGGAGGAGCTGCTCAGCACCAAGGTCACCCAGGAACT-GACGTAAGT 2668

Qy         60 ------------------------------------------------------------ 60

Db       2669 GCCCACCCGACTCCCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCCTGACCCTCCTGGCGA 2728

Qy         60 ------------------------------------------------------------ 60

Db       2729 ACCGTGTGTTCTGGACCCTCAGGCTCCACCCGTCCGGGTTTCCTTCTGTCCTTGTCGCCA 2788

Qy         60 ------------------------------------------------------------ 60

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Qy         60 ------------------------------------------------------------ 60

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Qy         60 ------------------------------------------------------------ 60

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Qy         61 ------ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeu 78

Db       3029 GCGCCCAGGGAGCTGATAGAGGAGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTG 3088

Qy         79 GluGluGlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGln 98

Db       3089 GAGGCGCAGCTGGGCCCCGTGACCCAGGAGACGCAGGCGCGCCTGTCCAAGGAGCTGCAG 3148

Qy         99 AlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyr 118

Db       3149 GCGGCGCAGGCCCGCGTGGGCGCCGACATGGAGGACGTGCGCAACCGCTTGGTGCTCTAC 3208

Qy        119 ArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAla 138

Db       3209 CGCAGCGAGGTGCACAACATGTTGGGCCAGACCACCGAGGAGCTGCGGAGCCGCCTGGCT 3268

Qy        139 SerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArg 158

Db       3269 TCCCACCTGCGCAAGCTGCGCAAGCGGCTGCTCCGCGACACCGAGGACCTGCAGAAGCGC 3328

Qy        159 LeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArg 178

Db       3329 CTGGCCGTGTACCAGGCGGGGCTGCGCGAGGGCGCCGAGCGCAGCGTGAGCGCCCTCCGC 3388

Qy        179 GluArgLeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeu 198

Db       3389 GAGCGCCTCGGGCCCCTGGTGGAGCAGGGCCGATTGCGCGCCGCCACCCTGAGTACCAGG 3448

Qy        199 AlaGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMet 218

Db       3449 GCCGGCCAGCCGCTGCGCGAGCGCGCGGAAGCCTGGGGCCAGAAGCTGCGCGGACGGCTG 3508

Qy        219 GluGluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu 238

Db       3509 GAGGAGATGGGCAGCCGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAG 3568

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Db       3569 GTGCGCACCAAAGTGGAGGAGCAGGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCAC 3628
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Qy        259 AlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGly 278
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Db       3629 GCCCTCCTCAAAGGCTGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCGGG 3688

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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 21:46:34 ; Search time 2158.08 Seconds
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Perfect score: 1493
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1493	100.0	1147	7	US-10-257-021-63	Sequence 63, Appl
2	1493	100.0	1156	3	US-09-827-854-8	Sequence 8, Appli
3	1493	100.0	1156	3	US-09-870-759-129	Sequence 129, App
4	1493	100.0	1156	3	US-09-802-640-17	Sequence 17, Appl
5	1493	100.0	1156	3	US-09-751-708A-129	Sequence 129, App
6	1493	100.0	1156	7	US-10-301-822-5	Sequence 5, Appli
7	1493	100.0	1156	7	US-10-313-641-1	Sequence 1, Appli
8	1493	100.0	1156	7	US-10-403-902A-17	Sequence 17, Appl
9	1493	100.0	1156	7	US-10-428-551-1	Sequence 1, Appli
10	1493	100.0	1156	8	US-10-641-643-1007	Sequence 1007, Ap
11	1493	100.0	1156	9	US-10-428-817A-125	Sequence 125, App
12	1493	100.0	1156	9	US-10-794-198A-1	Sequence 1, Appli
13	1493	100.0	1156	10	US-10-852-335A-10	Sequence 10, Appl
14	1493	100.0	1156	10	US-10-937-758A-106	Sequence 106, App
15	1493	100.0	1156	10	US-10-773-446-63	Sequence 63, Appl
16	1493	100.0	1156	15	US-11-186-284-5	Sequence 5, Appli
17	1493	100.0	1156	15	US-11-055-309A-1	Sequence 1, Appli
18	1493	100.0	1186	10	US-10-929-182-34	Sequence 34, Appl
19	1493	100.0	1291	3	US-09-919-039-246	Sequence 246, App
20	1493	100.0	1291	6	US-10-044-090-454	Sequence 454, App
21	1493	100.0	1291	6	US-10-116-802-256	Sequence 256, App
22	1493	100.0	1428	9	US-10-723-860-8338	Sequence 8338, Ap
23	1489	99.7	1156	3	US-09-827-854-12	Sequence 12, Appl
24	1485	99.5	1156	3	US-09-827-854-9	Sequence 9, Appli
25	1485	99.5	1156	3	US-09-827-854-11	Sequence 11, Appl
26	1484	99.4	1157	3	US-09-954-456-760	Sequence 760, App
27	1484	99.4	1157	3	US-09-880-107-2244	Sequence 2244, Ap
28	1484	99.4	1157	3	US-09-960-706-655	Sequence 655, App
29	1484	99.4	1157	3	US-09-873-319-409	Sequence 409, App
30	1484	99.4	1157	7	US-10-313-641-3	Sequence 3, Appli
31	1484	99.4	1157	7	US-10-428-551-3	Sequence 3, Appli
32	1484	99.4	1157	8	US-10-240-425-1291	Sequence 1291, Ap
33	1484	99.4	1157	9	US-10-723-860-4536	Sequence 4536, Ap
34	1484	99.4	1157	9	US-10-794-198A-3	Sequence 3, Appli
35	1484	99.4	1157	10	US-10-843-641A-3787	Sequence 3787, Ap
36	1484	99.4	1157	15	US-11-055-309A-3	Sequence 3, Appli
37	1481	99.2	1156	3	US-09-827-854-7	Sequence 7, Appli
38	1480	99.1	1220	16	US-11-091-883-126	Sequence 126, App
39	1480	99.1	1497	3	US-09-971-392-104	Sequence 104, App
c 40	1480	99.1	1497	7	US-10-252-157-265	Sequence 265, App
41	1478	99.0	1156	3	US-09-827-854-10	Sequence 10, Appl
42	1465	98.1	1372	9	US-10-741-600-475	Sequence 475, App
43	1389.5	93.1	1279	7	US-10-291-265-3	Sequence 3, Appli
44	1389.5	93.1	1279	15	US-11-000-463-3	Sequence 3, Appli
45	1378	92.3	1372	8	US-10-741-601-154	Sequence 154, App

ALIGNMENTS

RESULT 1
US-10-257-021-63
; Sequence 63, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-63

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Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
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Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        220 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 279

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
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Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
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RESULT 2
US-09-827-854-8
; Sequence 8, Application US/09827854
; Patent No. US20020123093A1
; GENERAL INFORMATION:
;  APPLICANT: Zannis, Vassilis
;  APPLICANT:  Kypreos, Kyriakos E.
;  TITLE OF INVENTION: Compounds and methods for lowering
;  TITLE OF INVENTION:  cholesterol  levels without inducing hypertriglyceridemia
;  FILE REFERENCE: 07180/004003
;  CURRENT APPLICATION NUMBER: US/09/827,854
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: US 09/679,088
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 09/544,386
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-854-8

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Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
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Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
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Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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RESULT 3
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; Sequence 129, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 870759
;  CURRENT APPLICATION NUMBER: US/09/870,759
;  CURRENT FILING DATE:  2002-01-14
;  PRIOR APPLICATION NUMBER: US 60/208,128
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 166
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(1014)
;   OTHER INFORMATION:
US-09-870-759-129

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-09-827-854A-2 (1-299) x US-09-870-759-129 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 4
US-09-802-640-17
; Sequence 17, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bonsal Aruna
;  APPLICANT:  Kleyn Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048
;  CURRENT APPLICATION NUMBER: US/09/802,640
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)...(1014)
;   OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein E
;   OTHER INFORMATION: (APOE)
US-09-802-640-17

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0
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US-09-827-854A-2 (1-299) x US-09-802-640-17 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 5
US-09-751-708A-129
; Sequence 129, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 751708
;  CURRENT APPLICATION NUMBER: US/09/751,708A
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 60/173,371
;  PRIOR FILING DATE: 1999-12-28
;  NUMBER OF SEQ ID NOS: 166
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(1014)
;   OTHER INFORMATION:
US-09-751-708A-129

Alignment Scores:
Pred. No.:                9.78e-135       Length:          1156
Score:                    1493.00         Matches:         299
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       3               Gaps:            0

US-09-827-854A-2 (1-299) x US-09-751-708A-129 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 6
US-10-301-822-5
; Sequence 5, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Berger, Allison
;  APPLICANT:  Guillemette, Tracy L.
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Thibodeau, Stephen N.
;  APPLICANT:  Burgart, Lawrence J.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF COLON CANCER
;  FILE REFERENCE: MPM01-029P2RNM
;  CURRENT APPLICATION NUMBER: US/10/301,822
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 60/339,971
;  PRIOR FILING DATE: 2001-12-10
;  PRIOR APPLICATION NUMBER: US 60/361,978
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/381,988
;  PRIOR FILING DATE: 2002-05-20
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)...(1014)
US-10-301-822-5

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-2 (1-299) x US-10-301-822-5 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 7
US-10-313-641-1
; Sequence 1, Application US/10313641
; Publication No. US20030162758A1
; GENERAL INFORMATION:
;  APPLICANT: Ishida, Brian
;  APPLICANT:  Duncan, Keith
;  APPLICANT:  Bailey, Kathy
;  APPLICANT:  Kane, John
;  APPLICANT:  Schwartz, Daniel
;  TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)
;  FILE REFERENCE: P02351US2
;  CURRENT APPLICATION NUMBER: US/10/313,641
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/415,864
;  PRIOR FILING DATE: 2002-10-03
;  PRIOR APPLICATION NUMBER: US 60/340,498
;  PRIOR FILING DATE: 2001-12-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Human
US-10-313-641-1

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-2 (1-299) x US-10-313-641-1 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 8
US-10-403-902A-17
; Sequence 17, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bansal, Aruna
;  APPLICANT:  Kleyn, Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048B
;  CURRENT APPLICATION NUMBER: US/10/403,902A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: 09/802,640
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)...(1014)
;   OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein E
;   OTHER INFORMATION: (APOE)
US-10-403-902A-17

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-2 (1-299) x US-10-403-902A-17 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 9
US-10-428-551-1
; Sequence 1, Application US/10428551
; Publication No. US20030229062A1
; GENERAL INFORMATION:
;  APPLICANT: Ishida, Brian
;  APPLICANT:  Duncan, Keith
;  APPLICANT:  Bailey, Kathy
;  APPLICANT:  Kane, John
;  APPLICANT:  Schwartz, Daniel
;  TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)
;  FILE REFERENCE: P02351US3
;  CURRENT APPLICATION NUMBER: US/10/428,551
;  CURRENT FILING DATE:  2003-05-02
;  PRIOR APPLICATION NUMBER: US 60/415,864
;  PRIOR FILING DATE: 2002-10-03
;  PRIOR APPLICATION NUMBER: US 60/340,498
;  PRIOR FILING DATE: 2001-12-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Human
US-10-428-551-1

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-2 (1-299) x US-10-428-551-1 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 10
US-10-641-643-1007
; Sequence 1007, Application US/10641643
; Publication No. US20040077003A1
;  GENERAL INFORMATION:
;       APPLICANT: Cocks, Benjamin G.
;                  Susan G. Stuart
;                  Jeffrey J. Seilhamer
;       TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                           GENE EXPRESSION
;       NUMBER OF SEQUENCES: 1508
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;            STREET: 3174 PORTER DRIVE
;            CITY: PALO ALTO
;            STATE: CALIFORNIA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/641,643
;            FILING DATE: 14-Aug-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Zeller, Karen J.
```

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;             REGISTRATION NUMBER: 37,071
;             REFERENCE/DOCKET NUMBER: PA-0001 US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 855-0555
;             TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1007:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1156 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: g178850
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1007 :
US-10-641-643-1007

Alignment Scores:
Pred. No.:                9.78e-135       Length:          1156
Score:                    1493.00         Matches:         299
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       8               Gaps:            0

US-09-827-854A-2 (1-299) x US-10-641-643-1007 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 11
US-10-428-817A-125
; Sequence 125, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 38373-189118
;  CURRENT APPLICATION NUMBER: US/10/428,817A
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: US 60/378,988
;  PRIOR FILING DATE: 2002-05-08
;  PRIOR APPLICATION NUMBER: US 60/389,366
;  PRIOR FILING DATE: 2002-06-15
;  PRIOR APPLICATION NUMBER: US 60/406,697
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: US 60/406,750
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/415,310
;  PRIOR FILING DATE: 2002-10-01
;  PRIOR APPLICATION NUMBER: US 60/415,400
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/438,686
;  PRIOR FILING DATE: 2003-01-09
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
;  LENGTH: 1156
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (61)..(1014)
US-10-428-817A-125

Alignment Scores:
Pred. No.:                9.78e-135       Length:          1156
Score:                    1493.00         Matches:         299
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       9               Gaps:            0

US-09-827-854A-2 (1-299) x US-10-428-817A-125 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
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RESULT 12
US-10-794-198A-1
; Sequence 1, Application US/10794198A
; Publication No. US20040266663A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: METHODS TO INCREASE REVERSE CHOLESTEROL TRANSPORT IN THE RETINAL
; TITLE OF INVENTION: EPITHELIUM (RPE) AND BRUCH'S MEMBRANE (BM)
; FILE REFERENCE: HO-P02351US4
; CURRENT APPLICATION NUMBER: US/10/794,198A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: HUMAN
US-10-794-198A-1

Alignment Scores:

Pred. No.:	9.78e-135	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-09-827-854A-2 (1-299) x US-10-794-198A-1 (1-1156)

```
Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
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RESULT 13
US-10-852-335A-10
; Sequence 10, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
;  APPLICANT: HEIDI S. PHILLIPS
;  TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
;  TITLE OF INVENTION:  Treatment of Tumors of Glial Origin
;  FILE REFERENCE: P5103R1-US
;  CURRENT APPLICATION NUMBER: US/10/852,335A
;  CURRENT FILING DATE:  2004-05-24
;  PRIOR APPLICATION NUMBER: US 60/548,299
;  PRIOR FILING DATE: 2004-02-27
;  PRIOR APPLICATION NUMBER: US 60/473,238
;  PRIOR FILING DATE: 2003-05-23
;  NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 10
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-852-335A-10

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-09-827-854A-2 (1-299) x US-10-852-335A-10 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011

RESULT 14
US-10-937-758A-106
; Sequence 106, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: FILE REFERENCE 650884
;  CURRENT APPLICATION NUMBER: US/10/937,758A
;  CURRENT FILING DATE:  2004-09-08
;  PRIOR APPLICATION NUMBER: 09/650,884
;  PRIOR FILING DATE: 2000-08-30
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(1014)
;   OTHER INFORMATION:
US-10-937-758A-106

Alignment Scores:
Pred. No.:              9.78e-135       Length:         1156
Score:                  1493.00         Matches:        299
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-09-827-854A-2 (1-299) x US-10-937-758A-106 (1-1156)

Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414
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Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
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RESULT 15
US-10-773-446-63
; Sequence 63, Application US/10773446
; Publication No. US20050176662A1
; GENERAL INFORMATION:
; APPLICANT: INANA, GEORGE
; APPLICANT: McLAREN, MARGARET
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 39532-192229
; CURRENT APPLICATION NUMBER: US/10/773,446
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-773-446-63

Alignment Scores:

Pred. No.:	9.78e-135	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
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US-09-827-854A-2 (1-299) x US-10-773-446-63 (1-1156)

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Qy          1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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Db        115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG 174

Qy         21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db        175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 234

Qy         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db        235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 294

Qy         61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354

Qy         81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db        355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCG 414

Qy        101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db        415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474

Qy        121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Db        475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 534

Qy        141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594

Qy        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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Db        595 GTGTACCAGGCCGGGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGC 654

Qy        181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714

Qy        201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAG 774

Qy        221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db        775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834

Qy        241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894

Qy        261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954

Qy        281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCGCCCCTGTGCCCAGCGACAATCAC 1011
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Search completed: June 15, 2006, 00:44:28
Job time : 2165.08 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:13 ; Search time 557.375 Seconds
(without alignments)
3097.698 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTFLAGCQA 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92	100.0	71	2	I15467	I15467 Sequence 10
2	92	100.0	71	2	I69313	I69313 Sequence 10
3	92	100.0	93	2	AR211787	AR211787 Sequence
4	92	100.0	117	8	ASTOOL10	Y09270 Artificial
5	92	100.0	275	5	HSJ2127	Z70760 H.sapiens m
6	92	100.0	405	2	BD025884	BD025884 Sequence
7	92	100.0	405	2	AR726145	AR726145 Sequence
8	92	100.0	405	2	AX886274	AX886274 Sequence
c 9	92	100.0	478	2	AX330507	AX330507 Sequence
c 10	92	100.0	478	2	AX335168	AX335168 Sequence
c 11	92	100.0	478	2	AX409845	AX409845 Sequence
12	92	100.0	499	2	AX427528	AX427528 Sequence
13	92	100.0	583	2	AR578700	AR578700 Sequence
14	92	100.0	660	2	A62340	A62340 Sequence 28
15	92	100.0	660	2	A62342	A62342 Sequence 30
16	92	100.0	660	2	A62344	A62344 Sequence 32
17	92	100.0	660	2	AR075563	AR075563 Sequence
18	92	100.0	1107	2	BD084811	BD084811 Diagnosis
19	92	100.0	1110	2	E00359	E00359 cDNA coding
20	92	100.0	1110	2	E00823	E00823 DNA sequenc
21	92	100.0	1110	2	E08423	E08423 DNA coding
22	92	100.0	1147	2	AX302545	AX302545 Sequence
23	92	100.0	1156	2	BD004277	BD004277 Apo E hum
24	92	100.0	1156	2	BD004278	BD004278 Apo E hum
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27	92	100.0	1156	2	CQ785970	CQ785970 Sequence
28	92	100.0	1156	2	CQ875269	CQ875269 Sequence
29	92	100.0	1156	2	CQ896276	CQ896276 Sequence
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31	92	100.0	1156	2	CQ981476	CQ981476 Sequence
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33	92	100.0	1156	2	AR380462	AR380462 Sequence
34	92	100.0	1156	2	AX821568	AX821568 Sequence
35	92	100.0	1156	5	HUMAPOE3	K00396 Homo sapien
36	92	100.0	1157	2	DD166085	DD166085 Treatment
37	92	100.0	1157	2	I15975	I15975 Sequence 1
38	92	100.0	1157	2	AX333278	AX333278 Sequence
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42	92	100.0	1186	5	BC003557	BC003557 Homo sapi
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ALIGNMENTS

RESULT 1
I15467
LOCUS I15467 71 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 10 from patent US 5466593.
ACCESSION I15467
VERSION I15467.1 GI:1250375
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 71)
AUTHORS Shimomura,T., Yamada,K., Morimoto,Y., Kitamura,N. and Miyazawa,K.
TITLE Hepatocyte growth factor activating protease and gene encoding the protease
JOURNAL Patent: US 5466593-A 10 14-NOV-1995;
FEATURES Location/Qualifiers
source 1. .71
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

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Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

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DB:                    2             Gaps:          0

US-09-827-854A-13 (1-18) x I15467 (1-71)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65

RESULT 2
I69313
LOCUS       I69313                  71 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 10 from patent US 5677164.
ACCESSION   I69313
VERSION     I69313.1  GI:2831435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Shimomura,T., Yamada,K., Morimoto,Y., Kitamura,N. and Miyazawa,K.
  TITLE     Hepatocyte growth factor activating protease and gene encoding the
            protease
  JOURNAL   Patent: US 5677164-A 10 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .71
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                     /mol_type="unassigned DNA"
ORIGIN

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Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-09-827-854A-13 (1-18) x I69313 (1-71)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65

RESULT 3
AR211787
LOCUS       AR211787                93 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6399371.
ACCESSION   AR211787
VERSION     AR211787.1  GI:21515202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Falduto,M.T., Magnuson,S.R. and Morgan,D.W.
  TITLE     Human matrix metalloprotease gene, proteins encoded therefrom and
            methods of using same
  JOURNAL   Patent: US 6399371-A 4 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .93
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                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.77e-09       Length:         93
Score:                  92.00          Matches:        18
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Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-09-827-854A-13 (1-18) x AR211787 (1-93)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69

RESULT 4
ASTOOL10
LOCUS       ASTOOL10                117 bp    DNA     linear   SYN 08-NOV-1996
DEFINITION  Artificial sequence DNA for expression cassette, toolbox 10.
ACCESSION   Y09270
VERSION     Y09270.1  GI:1666292
KEYWORDS    expression cassette; toolbox 10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schluesener,H.J.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 117)
  AUTHORS   Schluesener,H.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1996) H.J. Schluesener, Inst.f. Hirnforschung,
            Calwer Str. 3, D- 77076 Tuebingen, FRG
FEATURES             Location/Qualifiers
     source          1. .117
                     /organism="synthetic construct"
                     /mol_type="other DNA"
                     /db_xref="taxon:32630"
     CDS             1. .117
                     /codon_start=1
                     /transl_table=11
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ORIGIN

Alignment Scores:
Pred. No.:              3.49e-09       Length:         117
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     8              Gaps:           0

US-09-827-854A-13 (1-18) x ASTOOL10 (1-117)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTCGCAGGATGCCAGGCC 54

RESULT 5
HSJ2127
LOCUS       HSJ2127                 275 bp    mRNA    linear   PRI 18-APR-2005
DEFINITION  H.sapiens mRNA for apolipoprotein E (partial).
ACCESSION   Z70760
VERSION     Z70760.1  GI:1263122
KEYWORDS    apolipoprotein E.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Dmitrenko,V.V., Garifulin,O.M. and Kavsan,V.M.
  TITLE     Characterization of different mRNA types expressed in human brain
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 275)
  AUTHORS   Dmitrenko,V.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-1996) Dmitrenko V. V., Institute of Molecular
            Biology and Genetics, Biosynthesis of Nucleic Acids, Zabolotnogo
            150, Kiev, Ukraine, 252627
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FEATURES             Location/Qualifiers
     source          1. .275
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                     /db_xref="taxon:9606"
                     /clone="ICRFp507J2127"
                     /tissue_type="brain"
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                     /dev_stage="fetus"
     mRNA            1. .275
                     /standard_name="apolipoprotein E"
                     /note="homologous to K00396"
     5'UTR           1. .37
     CDS             38. .>275
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                     /db_xref="GI:1263123"
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                     /db_xref="InterPro:IPR000074"
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ORIGIN

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Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
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DB:                     5               Gaps:           0

US-09-827-854A-13 (1-18) x HSJ2127 (1-275)

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Db         38 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 91

RESULT 6
BD025884
LOCUS       BD025884                405 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD025884
VERSION     BD025884.1  GI:22567107
KEYWORDS    JP 2001269182-A/2130.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 2130 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/2130
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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            CC
            FH   Key             Location/Qualifiers
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ORIGIN

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Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x BD025884 (1-405)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128

RESULT 7
AR726145
LOCUS       AR726145                405 bp    DNA     linear   PAT 11-OCT-2005
DEFINITION  Sequence 2137 from patent US 6783961.
ACCESSION   AR726145
VERSION     AR726145.1  GI:77419885
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: US 6783961-A 2137 31-AUG-2004;
            Genset S.A.;;
            FRX;
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.22e-08        Length:         405
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x AR726145 (1-405)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128

RESULT 8
AX886274
LOCUS       AX886274                405 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2137 from Patent EP1033401.
ACCESSION   AX886274
VERSION     AX886274.1  GI:40043271
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 2137 06-SEP-2000;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .405
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                     /codon_start=1
                     /protein_id="CAF00412.1"
                     /db_xref="GI:40043272"
                     /translation="MPGQGGASGGDRAGARAAPZTEWQSGQRWELALGRFWDYLRWVQ
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ORIGIN

Alignment Scores:
Pred. No.:                1.22e-08        Length:         405
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x AX886274 (1-405)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128

RESULT 9
AX330507/c
LOCUS       AX330507                478 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 1016 from Patent WO0194629.
ACCESSION   AX330507
VERSION     AX330507.1  GI:18103485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 1016 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .478
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.44e-08        Length:         478
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x AX330507 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 10
AX335168/c
LOCUS       AX335168                478 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 5677 from Patent WO0194629.
ACCESSION   AX335168
VERSION     AX335168.1  GI:18125887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 5677 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .478
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                1.44e-08        Length:         478
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x AX335168 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 11
AX409845/c
LOCUS       AX409845                478 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 2492 from Patent WO0229103.
ACCESSION   AX409845
VERSION     AX409845.1  GI:21442550
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE     Gene expression profiles in liver cancer
  JOURNAL   Patent: WO 0229103-A 2492 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1. .478
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. N33009"
ORIGIN

Alignment Scores:
Pred. No.:                1.44e-08        Length:         478
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x AX409845 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 12
```

```
AX427528
LOCUS       AX427528                 499 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 38 from Patent WO0121836.
ACCESSION   AX427528
VERSION     AX427528.1  GI:21537674
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
            Bratcher, Shawn,R., Dufour,G.F., Cohen,H.J., Rosen,B.H., Shah,P.,
            Chalup,M.S., Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B.,
            Panzer,S.R., Roseberry,A.M., Wright,R.J., Chen,W., Liu,T.,
            Yap,P.E., Stockdreher,T.K., Amshey,S. and Fong,W.T.
  TITLE     Molecules for diagnostics and therapeutics
  JOURNAL   Patent: WO 0121836-A 38 29-MAR-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 346599.9.dec"
ORIGIN

Alignment Scores:
Pred. No.:              1.5e-08        Length:         499
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-09-827-854A-13 (1-18) x AX427528 (1-499)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 181

RESULT 13
AR578700
LOCUS       AR578700                 583 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 876 from patent US 6783969.
ACCESSION   AR578700
VERSION     AR578700.1  GI:56581496
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 583)
  AUTHORS   Tang,Y.T., Goodrich,R.W., Asundi,V. and Drmanac,R.T.
  TITLE     Cathepsin V-like polypeptides
  JOURNAL   Patent: US 6783969-A 876 31-AUG-2004;
            Nuvelo, Inc.; Sunnyvale, CA
FEATURES             Location/Qualifiers
     source          1. .583
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.76e-08       Length:         583
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-09-827-854A-13 (1-18) x AR578700 (1-583)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109

RESULT 14
A62340
LOCUS       A62340                   660 bp    DNA     linear   PAT 09-MAR-1998
DEFINITION  Sequence 28 from Patent WO9712992.
ACCESSION   A62340
VERSION     A62340.1  GI:3716293
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Van,L.F., Burbach,J.P. and Grosveld,F.G.
  TITLE     DIAGNOSIS METHOD AND REAGENTS
  JOURNAL   Patent: WO 9712992-A 28 10-APR-1997;
            ROYAL NETHERLANDS ACADEMY OF A (NL)
COMMENT     Other publication AU 7142796 970428.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             <2. .>660
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA03641.1"
                     /db_xref="GI:3716294"
                     /translation="PSGGEGRPSPGADWPITGRKMKVLWAALLVTFLAGCQAKVEQAV
                     ETEPEPELRQQTEWQSGQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALM
                     DETMKELKAYKSELEEQLTPVAEETRARLSKELQTAQARLGADMEDVCGRLVQYRGEV
                     QAMLGQSTEELRVRLASHLRKLRKRLLRDPDDLQKRLAVYQAGAREGAERGLSAIRER
                     LG"
ORIGIN

Alignment Scores:
Pred. No.:              1.99e-08       Length:         660
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-09-827-854A-13 (1-18) x A62340 (1-660)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115

RESULT 15
A62342
LOCUS       A62342                   660 bp    DNA     linear   PAT 09-MAR-1998
DEFINITION  Sequence 30 from Patent WO9712992.
ACCESSION   A62342
VERSION     A62342.1  GI:3716295
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Van,L.F., Burbach,J.P. and Grosveld,F.G.
  TITLE     DIAGNOSIS METHOD AND REAGENTS
  JOURNAL   Patent: WO 9712992-A 30 10-APR-1997;
            ROYAL NETHERLANDS ACADEMY OF A (NL)
COMMENT     Other publication AU 7142796 970428.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN
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Alignment Scores:

Pred. No.:	1.99e-08	Length:	660
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-09-827-854A-13 (1-18) x A62342 (1-660)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115
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Search completed: June 14, 2006, 21:46:04
Job time : 560.375 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 18:51:12 ; Search time 61.9495 Seconds
(without alignments)
3038.776 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTFLAGCQA 18

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: geneseqn1990s:*
3: geneseqn2000s:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92	100.0	79	10	ADE15845	Ade15845 Primer #1
2	92	100.0	93	2	AAV08172	Aav08172 Primer fo
3	92	100.0	93	6	ABL57678	Abl57678 Human mat
4	92	100.0	333	10	ACD95309	Acd95309 Human col
5	92	100.0	405	3	AAC02139	Aac02139 Human sec
6	92	100.0	407	6	ABK34238	Abk34238 Human cDN
7	92	100.0	440	14	ADV76096	Adv76096 Human col
8	92	100.0	441	14	ADV76095	Adv76095 Human col
9	92	100.0	445	9	ACH21663	Ach21663 Human adu
c 10	92	100.0	478	6	ABL67340	Abl67340 Thyroid c
c 11	92	100.0	478	6	ABL62679	Abl62679 Colon ade
c 12	92	100.0	478	6	ABN95994	Abn95994 Gene #249
13	92	100.0	480	10	ADJ57602	Adj57602 Human apo
14	92	100.0	499	4	AAS03049	Aas03049 Human dia
15	92	100.0	583	6	ABZ11994	Abz11994 Human pol
16	92	100.0	583	12	ADM44512	Adm44512 Novel hum
17	92	100.0	660	2	AAT69792	Aat69792 Partial h
18	92	100.0	684	12	ADG71903	Adg71903 Human cDN
19	92	100.0	684	12	ADJ87240	Adj87240 Human G p
20	92	100.0	709	12	ADG71915	Adg71915 Human cDN
21	92	100.0	709	12	ADJ87252	Adj87252 Human G p
22	92	100.0	718	12	ADG71909	Adg71909 Human cDN
23	92	100.0	718	12	ADJ87246	Adj87246 Human G p
24	92	100.0	788	12	ADG71907	Adg71907 Human cDN
25	92	100.0	788	12	ADJ87244	Adj87244 Human G p
26	92	100.0	802	12	ADG71905	Adg71905 Human cDN
27	92	100.0	802	12	ADJ87242	Adj87242 Human G p
28	92	100.0	954	6	AAD26035	Aad26035 Human apo
29	92	100.0	954	14	ADV42852	Adv42852 Human psy
30	92	100.0	1107	2	AAX75756	Aax75756 Human apo
31	92	100.0	1110	1	AAN50450	Aan50450 Sequence
32	92	100.0	1110	1	AAN60409	Aan60409 Human apo
33	92	100.0	1147	5	ABA83113	Aba83113 Apolipopr
34	92	100.0	1154	13	ADQ86961	Adq86961 Human tum
35	92	100.0	1156	4	AAF84315	Aaf84315 Human Apo
36	92	100.0	1156	4	AAF84314	Aaf84314 Human Apo
37	92	100.0	1156	4	AAF84316	Aaf84316 Human Apo
38	92	100.0	1156	6	ABT13008	Abt13008 Human apo
39	92	100.0	1156	6	AAD22052	Aad22052 Human apo
40	92	100.0	1156	6	AAD22047	Aad22047 Human apo
41	92	100.0	1156	6	AAD22048	Aad22048 Human apo
42	92	100.0	1156	6	AAD22051	Aad22051 Human apo
43	92	100.0	1156	6	AAD22049	Aad22049 Human apo
44	92	100.0	1156	6	AAD22050	Aad22050 Human apo
45	92	100.0	1156	8	ACA64743	Aca64743 Apolipopr

ALIGNMENTS

RESULT 1
ADE15845
ID ADE15845 standard; DNA; 79 BP.
XX
AC ADE15845;
XX
DT 29-JAN-2004 (first entry)
XX
DE Primer #12 of the invention.
XX
KW nicotinic acetylcholine receptor; AChR; Neuroprotective;
KW myasthenia gravis; ss; primer.
XX
OS Synthetic.
XX
PN WO2003087373-A2.
XX
PD 23-OCT-2003.
XX
PF 15-APR-2003; 2003WO-GR000014.
XX
PR 17-APR-2002; 2002GR-00100190.
XX
PA (HELL-) HELLENIC PASTEUR INST.
PA (ASFR-) ASSOC FR CONTRE MYOPATHIES.
PA (TZAR/) TZARTOS S.
PA (MAMA/) MAMALAKI A.

XX
PI Tzartos S, Mamalaki A, Psaridi-Linardaki L, Kostelidou K;
XX
DR WPI; 2003-903165/82.
XX
PT Producing recombinant domains of the human muscle nicotinic acetylcholine
PT receptor (AChR) for treating myasthenia gravis, which contains the major
PT part of the extracellular domain of the AChR receptor.
XX
PS Example 4; SEQ ID NO 13; 28pp; English.
XX
CC The present invention relates to producing of a group of recombinant
CC domains of the human muscle nicotinic acetylcholine receptor (AChR)
CC subunits alpha, beta, gamma, delta and epsilon, or the mutant forms of
CC the molecules, or the alpha domain containing the P3A exon, which
CC contains the major part of the extracellular domain of the receptor. The
CC method is useful for producing recombinant domains of the human muscle
CC nicotinic AChR for the immunoadsorption of anti-AChR antibodies in
CC myasthenia gravis patients. The permanently immobilized molecules can be
CC used either separately or in combination for therapeutic in vitro or ex
CC vivo elimination/apheresis of the majority of the anti-AChR antibodies
CC from the blood or sera of MG patients. The present sequence represents a
CC primer of the invention.
XX
SQ Sequence 79 BP; 13 A; 23 C; 27 G; 16 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.22e-07	Length:	79
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-09-827-854A-13 (1-18) x ADE15845 (1-79)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 62

RESULT 2
AAV08172
ID AAV08172 standard; DNA; 93 BP.
XX
AC AAV08172;
XX
DT 25-JAN-1999 (first entry)
XX
DE Primer for MMP19 coding sequence.
XX
KW MMP19; matrix metalloprotease 19; human; cancer; arthritis; inflammation;
KW therapy; diagnosis; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9840475-A1.
XX
PD 17-SEP-1998.
XX
PF 11-MAR-1998; 98WO-US004694.
XX
PR 11-MAR-1997; 97US-00814394.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Falduto M, Magnuson SR, Morgan DW;
XX
DR WPI; 1998-531521/45.
XX
PT New isolated human matrix metalloprotease gene - used to develop products
PT for the diagnosis, prevention and treatment of e.g. cancer, arthritis or
PT inflammation.
XX
PS Example 3; Page 49; 111pp; English.
XX
CC This sequence represents a PCR primer for the human matrix
CC metalloprotease 19 (MMP19) coding sequence of the invention. The DNA,
CC protein, and antibodies against MMP19 can be used in the diagnosis,
CC prognosis, prevention or treatment of individuals with conditions
CC associated with the expression of the MMP19 gene, such as cancer,
CC arthritis or inflammation, or to identify a predisposition to these
CC conditions. The DNA can be fixed to a substrate and used to detect the
CC presence of MMP19 in a sample. The sequences can be used to make primers
CC for use in reverse transcription PCR to detect MMP19, they can also be
CC used to identify inhibitors of MMP19
XX
SQ Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.1e-07	Length:	93
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-09-827-854A-13 (1-18) x AAV08172 (1-93)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69

RESULT 3
ABL57678
ID ABL57678 standard; DNA; 93 BP.
XX
AC ABL57678;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human matrix metalloprotease protein MMP-ABT EST upstream PCR primer #2.
XX
KW Human; MMP-ABT; matrix metalloprotease; cytostatic; anti-inflammatory;
KW anti-arthritic; gene therapy; cancer; inflammatory disease; arthritis;
KW EST; expressed sequence tag; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002031817-A1.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-1999; 99US-00391104.
XX
PR 11-MAR-1997; 97US-00814394.
XX
PA (FALD/) FALDUTO M T.
PA (MAGN/) MAGNUSON S R.
PA (MORG/) MORGAN D W.
XX
PI Falduto MT, Magnuson SR, Morgan DW;
XX
DR WPI; 2002-361182/39.
XX
PT New human matrix metalloprotease gene and protein, useful for diagnosing,
PT staging, preventing or treating cancer or inflammatory diseases (e.g.
PT arthritis), as well as in screening drugs for treating these diseases.
XX
PS Example 3; Page 23; 44pp; English.
XX
CC The sequence represents a PCR primer used in the invention to amplify DNA
CC encoding the clone 907334 matrix metalloprotease protein (MMP-ABT) from a
CC plasmid. The invention relates to a novel polynucleotide, which comprises
CC a nucleotide sequence encoding a human matrix metalloprotease protein
CC (designated MMP-ABT). The protein of the invention has cytostatic, anti-

CC inflammatory, and anti-arthritic activity. The polynucleotide may have a
CC use in gene therapy. The MMP-ABT polynucleotides and proteins are useful
CC for detecting, diagnosing, staging, monitoring, prognosing, preventing or
CC treating cancer or inflammatory diseases (e.g. arthritis). The MMP-ABT
CC proteins and polynucleotides are also useful developing therapeutic
CC agents that affect MMP function
XX
SQ Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.1e-07	Length:	93
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x ABL57678 (1-93)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69
```

RESULT 4
ACD95309
ID ACD95309 standard; cDNA; 333 BP.
XX
AC ACD95309;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #3721.
XX
KW Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
PS Example 9; Page 543; 959pp; English.
XX
CC The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA , sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 333 BP; 73 A; 83 C; 120 G; 55 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	2.26e-06	Length:	333
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-09-827-854A-13 (1-18) x ACD95309 (1-333)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 107
```

RESULT 5
AAC02139
ID AAC02139 standard; cDNA; 405 BP.
XX
AC AAC02139;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 2137.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR P-PSDB; AAG02133.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 2137; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 405 BP; 90 A; 105 C; 149 G; 60 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	2.85e-06	Length:	405
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-827-854A-13 (1-18) x AAC02139 (1-405)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128
```

RESULT 6
ABK34238
ID ABK34238 standard; cDNA; 407 BP.
XX
AC ABK34238;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human cDNA for novel secreted protein, SEQ ID 7.
XX
KW Human; ss; gene; secreted protein; immune deficiency; viral infection;
KW bacterial infection; fungal infection; autoimmune disorder; burn;
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW lymphoid cell deficiency.
XX
OS Homo sapiens.
XX
PN WO200177290-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US010295.
XX
PR 06-APR-2000; 2000US-0194941P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX
DR WPI; 2002-179323/23.
XX
PT Six hundred and twenty five polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.
XX
PS Claim 1; Page 70; 339pp; English.
XX
CC The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them. Also
CC included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the polynucleotides,
CC antibodies that bind to the proteins and identification of modulators of
CC the proteins or the expression of the polynucleotide. The polynucleotides
CC can be used as probes for the identification and isolation of full length
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
CC as nutritional supplements. The protein is useful in the treatment of
CC various immune deficiencies and disorders such as viral infections,
CC bacterial infections, fungal infections, autoimmune disorders (e.g.
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
CC tumours. They are also useful for tissue regeneration, for wound healing
CC and in the treatment of burns, incisions and ulcers. The proteins are
CC also useful for regulating haematopoiesis, for treating myeloid or
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
CC sequences encoding a secreted protein
XX
SQ Sequence 407 BP; 88 A; 103 C; 158 G; 58 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.86e-06	Length:	407
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x ABK34238 (1-407)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 73
```

RESULT 7
ADV76096
ID ADV76096 standard; DNA; 440 BP.
XX
AC ADV76096;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human colon tumor cell downregulated gene SEQ ID NO 2937.
XX
KW ds; gene; cancer; neoplasm; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004110345-A2.
XX
PD 23-DEC-2004.
XX
PF 28-OCT-2003; 2003WO-US034019.
XX
PR 29-OCT-2002; 2002US-0422176P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
PI Mazzarella RA, Staten NR;
XX
DR WPI; 2005-039958/04.
XX

PT New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 2937; 257pp; English.
XX
CC The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents a gene downregulated in human colon cancer
CC cells.
XX
SQ Sequence 440 BP; 94 A; 114 C; 168 G; 62 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	3.13e-06	Length:	440
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-09-827-854A-13 (1-18) x ADV76096 (1-440)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 110
```

RESULT 8
ADV76095
ID ADV76095 standard; DNA; 441 BP.
XX
AC ADV76095;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human colon tumor cell downregulated gene SEQ ID NO 2936.
XX
KW ds; gene; cancer; neoplasm; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004110345-A2.
XX
PD 23-DEC-2004.
XX
PF 28-OCT-2003; 2003WO-US034019.
XX
PR 29-OCT-2002; 2002US-0422176P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
PI Mazzarella RA, Staten NR;
XX
DR WPI; 2005-039958/04.
XX
PT New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 2936; 257pp; English.
XX
CC The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents a gene downregulated in human colon cancer
CC cells.
XX
SQ Sequence 441 BP; 98 A; 115 C; 166 G; 62 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.14e-06	Length:	441
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

US-09-827-854A-13 (1-18) x ADV76095 (1-441)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109
```

RESULT 9
ACH21663
ID ACH21663 standard; cDNA; 445 BP.
XX
AC ACH21663;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult ovary cDNA #43.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 8875; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 445 BP; 98 A; 113 C; 161 G; 72 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	3.18e-06	Length:	445
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-09-827-854A-13 (1-18) x ACH21663 (1-445)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 222
```

RESULT 10
ABL67340/c
ID ABL67340 standard; DNA; 478 BP.
XX
AC ABL67340;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5677.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 5677; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	3.45e-06	Length:	478
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x ABL67340 (1-478)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
```

RESULT 11
ABL62679/c
ID ABL62679 standard; DNA; 478 BP.
XX
AC ABL62679;
XX
DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1016.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.

XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 1016; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	3.45e-06	Length:	478
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US-09-827-854A-13 (1-18) x ABL62679 (1-478)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
```

RESULT 12
ABN95994/c
ID ABN95994 standard; DNA; 478 BP.
XX
AC ABN95994;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #2492 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 2492; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;

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Alignment Scores:
Pred. No.:              3.45e-06        Length:         478
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
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US-09-827-854A-13 (1-18) x ABN95994 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 13
ADJ57602
ID   ADJ57602 standard; DNA; 480 BP.
XX
AC   ADJ57602;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human apolipoprotein E DNA sequence.
XX
KW   SNP; single nucleotide polymorphism; gene expression; genotyping;
KW   apolipoprotein E; apoE; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003065146-A2.
XX
PD   07-AUG-2003.
XX
PF   02-JAN-2003; 2003WO-US000128.
XX
PR   25-JAN-2002; 2002US-0352039P.
PR   28-JAN-2002; 2002US-0352356P.
PR   01-APR-2002; 2002US-0369127P.
PR   03-APR-2002; 2002US-0369657P.
PR   09-APR-2002; 2002US-0370921P.
PR   26-APR-2002; 2002US-0376171P.
PR   06-MAY-2002; 2002US-0380057P.
PR   28-MAY-2002; 2002US-0383627P.
PR   29-MAY-2002; 2002US-0383954P.
PR   21-JUN-2002; 2002US-0390708P.
PR   05-JUL-2002; 2002US-0394115P.
PR   31-JUL-2002; 2002US-0399860P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Koehler RT,  Livak KJ,  Stevens J,  De La Vega FM,  Rhodes M;
PI   Bellon LR,  Dailey D,  Ziegle J,  Williams J,  Madden D,  Gilbert DA;
PI   Scafe CR,  Avi-Itzhak HI,  Webster MN,  Wang YN,  Spier EG,  You X;
PI   Hemken H,  Titus A,  Xu L,  Curlee J,  Heil J,  Glanowski S,  Scott J;
PI   Winn-Deen E,  Mccullen I,  Wu L,  Gire C,  Sprague A,  Eddins S;
XX
DR   WPI; 2003-679499/64.
DR   GENBANK; M10065.
XX
PT   Providing to consumer, assays for presence/expression of genetic
PT   material, by providing web-based user interface to receive order for
PT   stock assays, request for design and order for custom assays, and
PT   delivering assay.
XX
PS   Disclosure; Fig 9; 332pp; English.
XX
CC   The invention provides methods and assays for ordering assays which
CC   detect single nucleotide polymorphisms (SNPs) or gene expression. It
CC   provides to a consumer, assays to detect presence or expression of
CC   genetic material, by providing a web-based user interface to receive an
CC   order for one or more stock assays, providing a web-based user interface
CC   to receive a request for design of one or more custom assays and an order
CC   for the custom assays, and delivering to the consumer at least one custom
CC   or stock assay in response to the order. The methods use PCR and RT-PCR
CC   procedures. The present sequence represents a human apolipoprotein E
CC   (apoE) DNA sequence.
XX
SQ   Sequence 480 BP; 99 A; 137 C; 178 G; 66 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.47e-06        Length:         480
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
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DB:                     10              Gaps:           0

US-09-827-854A-13 (1-18) x ADJ57602 (1-480)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 114

RESULT 14
AAS03049
ID   AAS03049 standard; cDNA; 499 BP.
XX
AC   AAS03049;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human diagnostic and therapeutic (dithp) cDNA sequence #38.
XX
KW   Human diagnostic and therapeutic molecule; dithp; gene therapy;
KW   thalassemia; cardiovascular disorder; cell proliferative disorder;
KW   cancer; neurodegenerative disorder; autoimmune disorder;
KW   infectious disorder; inflammatory disorder; developmental disorder;
KW   Incyte ID number 3465999dec; secreted and extracellular molecule; ss.
XX
OS   Homo sapiens.
XX
PN   WO200121836-A2.
XX
PD   29-MAR-2001.
XX
PF   19-SEP-2000; 2000WO-US025643.
XX
PR   23-SEP-1999;   99US-0155760P.
PR   24-SEP-1999;   99US-0155939P.
PR   24-SEP-1999;   99US-0156294P.
PR   28-SEP-1999;   99US-0156565P.
PR   28-SEP-1999;   99US-0156624P.
PR   28-SEP-1999;   99US-0156625P.
PR   24-NOV-1999;   99US-0167410P.
PR   24-NOV-1999;   99US-0167517P.
PR   24-NOV-1999;   99US-0167520P.
PR   24-NOV-1999;   99US-0167521P.
PR   24-NOV-1999;   99US-0167522P.
PR   24-NOV-1999;   99US-0167542P.
PR   24-NOV-1999;   99US-0167543P.
PR   29-NOV-1999;   99US-0167943P.
PR   29-NOV-1999;   99US-0167945P.
PR   30-NOV-1999;   99US-0168197P.
PR   30-NOV-1999;   99US-0168265P.
PR   30-NOV-1999;   99US-0168429P.
PR   30-NOV-1999;   99US-0168432P.
PR   01-DEC-1999;   99US-0168468P.
PR   01-DEC-1999;   99US-0168599P.
PR   02-DEC-1999;   99US-0168611P.
PR   02-DEC-1999;   99US-0168613P.
PR   02-DEC-1999;   99US-0168857P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Hodgson DM,  Lincoln SE,  Russo FD,  Spiro PA,  Banville SC;
```

PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM;
PI Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK, Amshey S;
PI Fong WT;
XX
DR WPI; 2001-281607/29.
XX
PT Novel diagnostic and therapeutic polynucleotides, used in disease
PT diagnosis and for gene therapy of conditions such as cancer and
PT thalassemia.
XX
PS Claim 1; Page 274; 299pp; English.
XX
CC The present sequence for human diagnostic and therapeutic (dithp) cDNA
CC sequence #38 is 1 of 71 (AAS03012-AAS03082) novel sequences described in
CC the invention. The present sequence (Incyte ID No: 3465999dec) encodes a
CC secreted and extracellular molecule. The dithp polynucleotides may be
CC used to diagnose a condition disease or disorder associated with human
CC molecules. They can be used to identify the presence of similar nucleic
CC acids. Dithp polynucleotides may used to generate hybridisation probes
CC for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are
CC used to screen for molecules which bind to them and modulate their
CC activity. Dithp polynucleotides can be used for gene therapy of disorders
CC such as severe combined immunodeficiency syndrome (SCID), cystic
CC fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX
CC deficiencies, cardiovascular disorders e.g familial hypercholesterolaemia
CC (FH), cell proliferative disorders e.g. cancers, neurodegenerative
CC disorders, autoimmune/inflammatory disorders, infectious disorders and
CC developmental disorders. The antibodies can be used to analyse protein
CC expression levels
XX
SQ Sequence 499 BP; 107 A; 134 C; 189 G; 69 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.63e-06	Length:	499
Score:	92.00	Matches:	18
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Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x AAS03049 (1-499)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 181
```

RESULT 15
ABZ11994
ID ABZ11994 standard; cDNA; 583 BP.
XX
AC ABZ11994;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 876.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR P-PSDB; ABP69777.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 876; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 583 BP; 138 A; 154 C; 161 G; 130 T; 0 U; 0 Other;

Alignment Scores:

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Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x ABZ11994 (1-583)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109
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13: gb_gss3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	5	92	100.0	221	2	BF877344	BF877344 QV2-ET010
c	6	92	100.0	223	2	BF876758	BF876758 QV2-ET010
c	7	92	100.0	223	2	BF877285	BF877285 QV2-ET010
	8	92	100.0	227	2	BI039120	BI039120 IL3-NT028
	9	92	100.0	230	2	BI040603	BI040603 IL3-NT028
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	15	92	100.0	274	2	BF877232	BF877232 QV2-ET010
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c	22	92	100.0	344	1	AA962652	AA962652 or31f02.s
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	28	92	100.0	375	3	BQ684487	BQ684487 AGENCOURT
	29	92	100.0	377	10	DV770547	DV770547 ILLUMIGEN
c	30	92	100.0	381	1	AA769671	AA769671 ob19c01.s
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c	44	92	100.0	398	1	AI075319	AI075319 ou65h09.x
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ALIGNMENTS

RESULT 1
CN277418
LOCUS CN277418 125 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000417761214 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN277418
VERSION CN277418.1 GI:47293832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 125)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 125 Std Error: 0.00.

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                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from embryoid body outgrowths derived from hES cell lines
                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

Alignment Scores:
Pred. No.:              6.07e-06        Length:         125
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     8               Gaps:           0

US-09-827-854A-13 (1-18) x CN277418 (1-125)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 94

RESULT 2
BF877359
LOCUS       BF877359                177 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-161100-475-f12 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877359
VERSION     BF877359.1  GI:12267489
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 177)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            161100-475-f12&t3=2000-11-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 177.
FEATURES             Location/Qualifiers
     source          1. .177
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              9.21e-06        Length:         177
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x BF877359 (1-177)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 77

RESULT 3
CN277422
LOCUS       CN277422                216 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000600008337 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN277422
VERSION     CN277422.1  GI:47293836
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 216)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 216   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .216
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, DMSO-treated H9 cell
                     line"
                     /clone_lib="GRN_PREHEP"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from DMSO-treated hES cell line H9 (p22) maintained in
                     feeder-free conditions"
ORIGIN

Alignment Scores:
Pred. No.:              1.17e-05        Length:         216
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     8               Gaps:           0

US-09-827-854A-13 (1-18) x CN277422 (1-216)
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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 107

RESULT 4
BF877229/c
LOCUS       BF877229                221 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-151100-478-b01 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877229
VERSION     BF877229.1  GI:12267359
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 221)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            151100-478-b01&t3=2000-11-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 221.
FEATURES             Location/Qualifiers
     source          1. .221
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-05         Length:         221
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x BF877229 (1-221)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 142

RESULT 5
BF877344/c
LOCUS       BF877344                221 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-161100-475-b06 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877344
VERSION     BF877344.1  GI:12267474
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 221)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            161100-475-b06&t3=2000-11-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 221.
FEATURES             Location/Qualifiers
     source          1. .221
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-05         Length:         221
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x BF877344 (1-221)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db        195 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 142

RESULT 6
BF876758/c
LOCUS       BF876758                223 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-141100-474-g11 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF876758
VERSION     BF876758.1  GI:12266888
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 223)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            141100-474-g11&t3=2000-11-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 223.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-05        Length:          223
Score:                    92.00           Matches:         18
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       2               Gaps:            0

US-09-827-854A-13 (1-18) x BF876758 (1-223)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 144

RESULT 7
BF877285/c
LOCUS       BF877285                223 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-161100-474-g11 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877285
VERSION     BF877285.1  GI:12267415
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 223)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            161100-474-g11&t3=2000-11-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 223.
FEATURES             Location/Qualifiers
     source          1. .223
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-05        Length:          223
Score:                    92.00           Matches:         18
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       2               Gaps:            0

US-09-827-854A-13 (1-18) x BF877285 (1-223)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 144

RESULT 8
BI039120
LOCUS       BI039120                227 bp    mRNA    linear   EST 14-JUN-2001
DEFINITION  IL3-NT0280-240101-418-F05 NT0280 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI039120
VERSION     BI039120.1  GI:14445746
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 227)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
```

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            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-NT0280-
            240101-418-F05&t3=2001-01-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 227.
FEATURES             Location/Qualifiers
     source          1. .227
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0280"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.24e-05        Length:         227
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x BI039120 (1-227)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 55

RESULT 9
BI040603
LOCUS       BI040603                230 bp    mRNA    linear   EST 14-JUN-2001
DEFINITION  IL3-NT0280-090201-454-D05 NT0280 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI040603
VERSION     BI040603.1  GI:14447229
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 230)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-NT0280-
            090201-454-D05&t3=2001-02-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 230.
FEATURES             Location/Qualifiers
     source          1. .230
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="NT0280"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:                1.26e-05        Length:         230
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x BI040603 (1-230)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db          2 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 55

RESULT 10
CN277423
LOCUS       CN277423                243 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000425248791 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN277423
VERSION     CN277423.1  GI:47293837
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 243)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 243   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .243
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Alignment Scores:

Pred. No.:	1.35e-05	Length:	243
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-09-827-854A-13 (1-18) x CN277423 (1-243)

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Db         72 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 125
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RESULT 11
BE164869
LOCUS BE164869 256 bp mRNA linear EST 21-JUN-2000
DEFINITION QV1-HT0471-270300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE164869
VERSION BE164869.1 GI:8627590
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV1-HT0471-270300-121-f07&t3=2000-03-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 256.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0471"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	1.43e-05	Length:	256
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-09-827-854A-13 (1-18) x BE164869 (1-256)

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Db         17 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 70
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RESULT 12
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LOCUS BE164912 256 bp mRNA linear EST 21-JUN-2000
DEFINITION QV1-HT0471-280300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE164912
VERSION BE164912.1 GI:8627633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV1-HT0471-280300-121-f07&t3=2000-03-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 256.

FEATURES Location/Qualifiers
source 1. .256
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0471"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

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Pred. No.:              1.43e-05        Length:         256
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-13 (1-18) x BE164912 (1-256)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         17 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 70

RESULT 13
CB153811
LOCUS       CB153811                269 bp    mRNA    linear   EST 29-JAN-2003
DEFINITION  K-EST0211405 L17N670205 Homo sapiens cDNA clone L17N670205-6-G09
            5', mRNA sequence.
ACCESSION   CB153811
VERSION     CB153811.1  GI:28138807
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 269)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 6  row: G  column: 09
            High quality sequence stop: 269.
FEATURES             Location/Qualifiers
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                     /sex="F"
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                     /clone_lib="L17N670205"
                     /note="Organ: Liver; Vector: pT7T3D-PacI; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

Alignment Scores:
Pred. No.:              1.52e-05        Length:         269
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     4               Gaps:           0

US-09-827-854A-13 (1-18) x CB153811 (1-269)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         45 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 98

RESULT 14
BF877186
LOCUS       BF877186                273 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-151100-477-f05 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877186
VERSION     BF877186.1  GI:12267316
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 273)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-
            151100-477-f05&t3=2000-11-15&t4=1)
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            High quality sequence stop: 273.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="ET0106"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Alignment Scores:
Pred. No.:              1.55e-05        Length:         273
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-09-827-854A-13 (1-18) x BF877186 (1-273)

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Db         25 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 78

RESULT 15
BF877232
LOCUS       BF877232                274 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  QV2-ET0106-151100-478-c04 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF877232
VERSION     BF877232.1  GI:12267362
KEYWORDS    EST.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 274)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-151100-478-c04&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 274.
FEATURES Location/Qualifiers
source 1. .274
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0106"
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN

Alignment Scores:

Pred. No.:	1.55e-05	Length:	274
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-09-827-854A-13 (1-18) x BF877232 (1-274)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         26 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 79
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Search completed: June 15, 2006, 00:06:04
Job time : 479.517 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:03:31 ; Search time 18.795 Seconds
(without alignments)
2687.952 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTFLAGCQA 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-HOST=abss04 -USER=US09827854_@CGN_1_1_252_@runat_14062006_081830_26810
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	92	100.0	71	2	US-08-148-910-10	Sequence 10, Appl
	2	92	100.0	71	2	US-08-448-937A-10	Sequence 10, Appl
	3	92	100.0	93	3	US-09-391-104-4	Sequence 4, Appli
	4	92	100.0	405	3	US-09-513-999C-2137	Sequence 2137, Ap
c	5	92	100.0	478	4	US-09-880-107-2491	Sequence 2491, Ap
	6	92	100.0	583	3	US-09-799-451-876	Sequence 876, App
	7	92	100.0	660	2	US-08-726-306A-28	Sequence 28, Appl
	8	92	100.0	684	4	US-10-211-689-29	Sequence 29, Appl
	9	92	100.0	709	4	US-10-211-689-41	Sequence 41, Appl
	10	92	100.0	718	4	US-10-211-689-35	Sequence 35, Appl
	11	92	100.0	788	4	US-10-211-689-33	Sequence 33, Appl
	12	92	100.0	802	4	US-10-211-689-31	Sequence 31, Appl
	13	92	100.0	1156	3	US-09-023-655-1007	Sequence 1007, Ap
	14	92	100.0	1157	2	US-07-709-949-1	Sequence 1, Appli
	15	92	100.0	1157	4	US-09-880-107-2244	Sequence 2244, Ap
	16	92	100.0	1291	3	US-09-919-039-246	Sequence 246, App
	17	87	94.6	616	4	US-10-211-689-39	Sequence 39, Appl
	18	87	94.6	691	4	US-10-211-689-45	Sequence 45, Appl
	19	84	91.3	372	3	US-09-621-976-1386	Sequence 1386, Ap
	20	75	81.5	3805	3	US-09-108-006C-3	Sequence 3, Appli
	21	68	73.9	1126	3	US-08-949-155-5	Sequence 5, Appli
	22	68	73.9	1126	3	US-09-819-964-5	Sequence 5, Appli
	23	58	63.0	4267	3	US-08-949-155-51	Sequence 51, Appl
	24	58	63.0	4267	3	US-09-819-964-51	Sequence 51, Appl
c	25	54	58.7	183	3	US-09-489-039A-7011	Sequence 7011, Ap
	26	54	58.7	645	3	US-09-489-039A-7153	Sequence 7153, Ap
	27	53	57.6	303	3	US-09-252-991A-2604	Sequence 2604, Ap
c	28	53	57.6	6285	3	US-09-949-016-12815	Sequence 12815, A
c	29	53	57.6	6286	3	US-09-949-016-17179	Sequence 17179, A
c	30	53	57.6	6794	3	US-09-902-540-736	Sequence 736, App
	31	50	54.3	1143	3	US-09-902-540-3531	Sequence 3531, Ap
c	32	50	54.3	18538	3	US-09-902-540-1169	Sequence 1169, Ap
c	33	48.5	52.7	367	3	US-09-513-999C-2304	Sequence 2304, Ap
	34	48	52.2	3909	2	US-08-232-537-1	Sequence 1, Appli
	35	47	51.1	576	3	US-09-252-991A-9976	Sequence 9976, Ap
c	36	47	51.1	670689	3	US-09-949-016-12505	Sequence 12505, A
c	37	47	51.1	670690	3	US-09-949-016-14207	Sequence 14207, A
	38	46	50.0	601	3	US-09-949-016-197665	Sequence 197665,
	39	46	50.0	2665	3	US-09-902-540-3712	Sequence 3712, Ap
	40	46	50.0	18031	3	US-09-902-540-1180	Sequence 1180, Ap
	41	46	50.0	54444	3	US-09-949-016-17344	Sequence 17344, A
c	42	46	50.0	109690	3	US-09-949-016-13525	Sequence 13525, A
c	43	45.5	49.5	601	3	US-09-949-016-118246	Sequence 118246,
c	44	45.5	49.5	57507	3	US-09-949-016-15019	Sequence 15019, A
c	45	45	48.9	438	3	US-09-902-540-1579	Sequence 1579, Ap

ALIGNMENTS

RESULT 1
US-08-148-910-10
; Sequence 10, Application US/08148910
; Patent No. 5466593
; GENERAL INFORMATION:
; APPLICANT: Takeshi SHIMOMURA et al.
; TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch,
; MEDIUM TYPE: 500 Kb Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,910
; FILING DATE: No. 5466593ember 5, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
;    ORIGINAL SOURCE:
;      ORGANISM:  human
US-08-148-910-10

Alignment Scores:
Pred. No.:                1.54e-08        Length:         71
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x US-08-148-910-10 (1-71)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         12 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65

RESULT 2
US-08-448-937A-10
; Sequence 10, Application US/08448937A
; Patent No. 5677164
;  GENERAL INFORMATION:
;    APPLICANT:  Takeshi SHIMOMURA et al.
;    TITLE OF INVENTION:  No. 5677164el Protein and Gene Encoding Said Protein
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch,
;      MEDIUM TYPE:  500 Kb Storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,937A
;      FILING DATE:  May 24, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/148,910
;      FILING DATE:  No. 5677164ember 5, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid (synthetic DNA)
;    ORIGINAL SOURCE:
;      ORGANISM:  human
US-08-448-937A-10

Alignment Scores:
Pred. No.:                1.54e-08        Length:         71
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       2               Gaps:           0

US-09-827-854A-13 (1-18) x US-08-448-937A-10 (1-71)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65

RESULT 3
US-09-391-104-4
; Sequence 4, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 93
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Upstream primer
US-09-391-104-4

Alignment Scores:
Pred. No.:                2.13e-08        Length:         93
Score:                    92.00           Matches:        18
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       3               Gaps:           0

US-09-827-854A-13 (1-18) x US-09-391-104-4 (1-93)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69

RESULT 4
US-09-513-999C-2137
; Sequence 2137, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
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;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 2137
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 119..403
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 176
;   OTHER INFORMATION: s=g or c
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 20
;   OTHER INFORMATION: Xaa=Glu or Gln
US-09-513-999C-2137

Alignment Scores:
Pred. No.:              1.26e-07       Length:         405
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-09-827-854A-13 (1-18) x US-09-513-999C-2137 (1-405)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128

RESULT 5
US-09-880-107-2491/c
; Sequence 2491, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2491
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. 6974667 N33009
;   NAME/KEY: unsure
;   LOCATION: (1)..(478)
;   OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2491

Alignment Scores:
Pred. No.:              1.54e-07       Length:         478
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     4              Gaps:           0

US-09-827-854A-13 (1-18) x US-09-880-107-2491 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 6
US-09-799-451-876
; Sequence 876, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Yamazaki, Victoria
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Reena
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6783969el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 803
;  CURRENT APPLICATION NUMBER: US/09/799,451
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 876
;   LENGTH: 583
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (100)..(423)
US-09-799-451-876

Alignment Scores:
Pred. No.:              1.96e-07       Length:         583
Score:                  92.00          Matches:        18
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     3              Gaps:           0

US-09-827-854A-13 (1-18) x US-09-799-451-876 (1-583)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109

RESULT 7
US-08-726-306A-28
; Sequence 28, Application US/08726306A
; Patent No. 5958684
;  GENERAL INFORMATION:
;    APPLICANT:  van Leeuwen, Frederik Willem
;    APPLICANT:  Burbach, Johannes Peter Henri
;    APPLICANT:  Grosveld, Franklin G.
;    TITLE OF INVENTION:  DIAGNOSIS METHOD AND REAGENTS
;    NUMBER OF SEQUENCES:  189
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1 Financial Center
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
```

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;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,306A
;      FILING DATE:  02-Oct-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 95/20080.4
;      FILING DATE:  02-Oct-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/009,832
;      FILING DATE:  01-Jan-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  96,048-A (3255/00784)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-726-306A-28

Alignment Scores:
Pred. No.:                2.28e-07        Length:          660
Score:                    92.00           Matches:         18
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       2               Gaps:            0

US-09-827-854A-13 (1-18) x US-08-726-306A-28 (1-660)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115

RESULT 8
US-10-211-689-29
; Sequence 29, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(599)
US-10-211-689-29

Alignment Scores:
Pred. No.:                2.38e-07        Length:          684
Score:                    92.00           Matches:         18
Percent Similarity:       100.0%          Conservative:    0
Best Local Similarity:    100.0%          Mismatches:      0
Query Match:              100.0%          Indels:          0
DB:                       4               Gaps:            0

US-09-827-854A-13 (1-18) x US-10-211-689-29 (1-684)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         18 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 71

RESULT 9
US-10-211-689-41
; Sequence 41, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
```

; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 41
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(709)
US-10-211-689-41

Alignment Scores:

Pred. No.:	2.48e-07	Length:	709
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-211-689-41 (1-709)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 67
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RESULT 10
US-10-211-689-35
; Sequence 35, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khramstov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(718)
US-10-211-689-35

Alignment Scores:

Pred. No.:	2.52e-07	Length:	718
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-211-689-35 (1-718)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 64
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RESULT 11
US-10-211-689-33
; Sequence 33, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khramstov, Nikolai V.
; APPLICANT: Lepley, Denise M.

; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 33
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(704)
US-10-211-689-33

Alignment Scores:

Pred. No.:	2.82e-07	Length:	788
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-211-689-33 (1-788)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 71
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RESULT 12
US-10-211-689-31
; Sequence 31, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khramstov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 31
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(716)
US-10-211-689-31

Alignment Scores:

Pred. No.:	2.88e-07	Length:	802
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-211-689-31 (1-802)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 71
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RESULT 13
US-09-023-655-1007
; Sequence 1007, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer

```
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1007:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1156 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g178850
US-09-023-655-1007

Alignment Scores:
Pred. No.:              4.48e-07      Length:         1156
Score:                  92.00         Matches:        18
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            100.0%        Indels:         0
DB:                     3             Gaps:           0

US-09-827-854A-13 (1-18) x US-09-023-655-1007 (1-1156)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 114

RESULT 14
US-07-709-949-1
; Sequence 1, Application US/07709949
; Patent No. 5472858
;  GENERAL INFORMATION:
;    APPLICANT:  Attie, Alan D
;    APPLICANT:  Gretch, Daniel G
;    APPLICANT:  Sturley, Stephen L
;    APPLICANT:  Beckage, Nancy E
;    TITLE OF INVENTION:  Production of Recombinant Proteins in
;    TITLE OF INVENTION:  Insect Larvae
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  P.O. Box 2113
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  USA
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/709,949
;      FILING DATE:  19910604
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27,386
;      REFERENCE/DOCKET NUMBER:  9629691801
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 251-5000
;      TELEFAX:  (608)251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1157 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  62..1015
;    FEATURE:
;      NAME/KEY:  misc_signal
;      LOCATION:  62..119
;    PUBLICATION INFORMATION:
;      AUTHORS:  McLean, J W
;      JOURNAL:  Journal of Biological Chemistry
;      VOLUME:  259
;      PAGES:  6498-6504
;      DATE:  1984
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 1157
US-07-709-949-1

Alignment Scores:
Pred. No.:              4.49e-07      Length:         1157
Score:                  92.00         Matches:        18
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            100.0%        Indels:         0
DB:                     2             Gaps:           0

US-09-827-854A-13 (1-18) x US-07-709-949-1 (1-1157)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115

RESULT 15
US-09-880-107-2244
; Sequence 2244, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
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; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 M12529
US-09-880-107-2244

Alignment Scores:

Pred. No.:	4.49e-07	Length:	1157
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-09-827-854A-13 (1-18) x US-09-880-107-2244 (1-1157)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115
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Search completed: June 14, 2006, 19:16:12
Job time : 20.795 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 21:46:34 ; Search time 129.918 Seconds
(without alignments)
2553.658 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTFLAGCQA 18

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/abss/ABSSWEB_spool/US09827854/runat_14062006_081838_26978/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	92	100.0	93	3	US-09-391-104-4	Sequence 4, Appli
	2	92	100.0	201	8	US-10-741-601-3278	Sequence 3278, Ap
	3	92	100.0	201	10	US-10-995-561-8950	Sequence 8950, Ap
	4	92	100.0	407	3	US-09-823-245A-7	Sequence 7, Appli
	5	92	100.0	440	9	US-10-696-639-2937	Sequence 2937, Ap
	6	92	100.0	441	9	US-10-696-639-2936	Sequence 2936, Ap
	7	92	100.0	445	3	US-09-918-995-8875	Sequence 8875, Ap
c	8	92	100.0	478	3	US-09-964-824A-374	Sequence 374, App
c	9	92	100.0	478	3	US-09-880-107-2491	Sequence 2491, Ap
c	10	92	100.0	478	3	US-09-873-367C-1016	Sequence 1016, Ap
c	11	92	100.0	478	10	US-10-843-641A-1016	Sequence 1016, Ap
c	12	92	100.0	478	10	US-10-843-641A-5677	Sequence 5677, Ap
	13	92	100.0	583	8	US-10-302-172-876	Sequence 876, App
	14	92	100.0	684	7	US-10-211-689-29	Sequence 29, Appl
	15	92	100.0	709	7	US-10-211-689-41	Sequence 41, Appl
	16	92	100.0	718	7	US-10-211-689-35	Sequence 35, Appl
	17	92	100.0	788	7	US-10-211-689-33	Sequence 33, Appl
	18	92	100.0	802	7	US-10-211-689-31	Sequence 31, Appl
	19	92	100.0	1147	7	US-10-257-021-63	Sequence 63, Appl
	20	92	100.0	1156	3	US-09-827-854-7	Sequence 7, Appli
	21	92	100.0	1156	3	US-09-827-854-8	Sequence 8, Appli
	22	92	100.0	1156	3	US-09-827-854-9	Sequence 9, Appli
	23	92	100.0	1156	3	US-09-827-854-10	Sequence 10, Appl
	24	92	100.0	1156	3	US-09-827-854-11	Sequence 11, Appl
	25	92	100.0	1156	3	US-09-827-854-12	Sequence 12, Appl
	26	92	100.0	1156	3	US-09-870-759-129	Sequence 129, App
	27	92	100.0	1156	3	US-09-802-640-17	Sequence 17, Appl
	28	92	100.0	1156	3	US-09-751-708A-129	Sequence 129, App
	29	92	100.0	1156	7	US-10-301-822-5	Sequence 5, Appli
	30	92	100.0	1156	7	US-10-313-641-1	Sequence 1, Appli
	31	92	100.0	1156	7	US-10-403-902A-17	Sequence 17, Appl
	32	92	100.0	1156	7	US-10-428-551-1	Sequence 1, Appli
	33	92	100.0	1156	8	US-10-641-643-1007	Sequence 1007, Ap
	34	92	100.0	1156	9	US-10-428-817A-125	Sequence 125, App
	35	92	100.0	1156	9	US-10-794-198A-1	Sequence 1, Appli
	36	92	100.0	1156	10	US-10-852-335A-10	Sequence 10, Appl
	37	92	100.0	1156	10	US-10-937-758A-106	Sequence 106, App
	38	92	100.0	1156	10	US-10-773-446-63	Sequence 63, Appl
	39	92	100.0	1156	15	US-11-186-284-5	Sequence 5, Appli
	40	92	100.0	1156	15	US-11-055-309A-1	Sequence 1, Appli
	41	92	100.0	1157	3	US-09-954-456-760	Sequence 760, App
	42	92	100.0	1157	3	US-09-880-107-2244	Sequence 2244, Ap
	43	92	100.0	1157	3	US-09-960-706-655	Sequence 655, App
	44	92	100.0	1157	3	US-09-873-319-409	Sequence 409, App
	45	92	100.0	1157	7	US-10-313-641-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-391-104-4
; Sequence 4, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Upstream primer

US-09-391-104-4

Alignment Scores:

Pred. No.:	4.91e-07	Length:	93
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-827-854A-13 (1-18) x US-09-391-104-4 (1-93)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69
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RESULT 2
US-10-741-601-3278
; Sequence 3278, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3278
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-3278

Alignment Scores:

Pred. No.:	1.18e-06	Length:	201
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-741-601-3278 (1-201)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 64
```

RESULT 3
US-10-995-561-8950
; Sequence 8950, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8950
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-8950

Alignment Scores:

Pred. No.:	1.18e-06	Length:	201
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-995-561-8950 (1-201)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 64
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RESULT 4
US-09-823-245A-7
; Sequence 7, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-7

Alignment Scores:

Pred. No.:	2.63e-06	Length:	407
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-827-854A-13 (1-18) x US-09-823-245A-7 (1-407)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 73
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RESULT 5
US-10-696-639-2937
; Sequence 2937, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2937
; LENGTH: 440
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (339)..(412)
; OTHER INFORMATION: n=unknown
US-10-696-639-2937

Alignment Scores:

Pred. No.:	2.87e-06	Length:	440
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-696-639-2937 (1-440)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 110
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RESULT 6
US-10-696-639-2936
; Sequence 2936, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2936
; LENGTH: 441
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-2936

Alignment Scores:

Pred. No.:	2.88e-06	Length:	441
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-696-639-2936 (1-441)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109
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RESULT 7
US-09-918-995-8875
; Sequence 8875, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8875
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(445)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8875

Alignment Scores:

Pred. No.:	2.91e-06	Length:	445
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-827-854A-13 (1-18) x US-09-918-995-8875 (1-445)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 222
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RESULT 8
US-09-964-824A-374/c
; Sequence 374, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 374
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(478)
; OTHER INFORMATION: n=a,t,g or c
US-09-964-824A-374

Alignment Scores:

Pred. No.:	3.16e-06	Length:	478
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-827-854A-13 (1-18) x US-09-964-824A-374 (1-478)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
```

RESULT 9
US-09-880-107-2491/c
; Sequence 2491, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.

```
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2491
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 N33009
;   NAME/KEY: unsure
;   LOCATION: (1)..(478)
;   OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2491

Alignment Scores:
Pred. No.:              3.16e-06        Length:         478
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-09-827-854A-13 (1-18) x US-09-880-107-2491 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 10
US-09-873-367C-1016/c
; Sequence 1016, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  APPLICANT:  Soppet, Daniel
;  APPLICANT:  Endress, Gregory
;  APPLICANT:  Augustus, Meena
;  APPLICANT:  Ebner, Reinhard
;  APPLICANT:  Carter, Kenneth
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-64
;  CURRENT APPLICATION NUMBER: US/09/873,367C
;  CURRENT FILING DATE:  2003-04-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,891
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,842
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/244,867
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: U.S. 60/245,084
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 1067
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1016
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(478)
;   OTHER INFORMATION: n=a,t,g or c
US-09-873-367C-1016

Alignment Scores:
Pred. No.:              3.16e-06        Length:         478
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-09-827-854A-13 (1-18) x US-09-873-367C-1016 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 11
US-10-843-641A-1016/c
; Sequence 1016, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1016
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(478)
;   OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-1016

Alignment Scores:
Pred. No.:              3.16e-06        Length:         478
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     10              Gaps:           0

US-09-827-854A-13 (1-18) x US-10-843-641A-1016 (1-478)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 12
US-10-843-641A-5677/c
; Sequence 5677, Application US/10843641A
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; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5677
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(478)
; OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-5677

Alignment Scores:

Pred. No.:	3.16e-06	Length:	478
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-843-641A-5677 (1-478)

```
Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
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RESULT 13
US-10-302-172-876
; Sequence 876, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids ar
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 876
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(423)
US-10-302-172-876

Alignment Scores:

Pred. No.:	3.96e-06	Length:	583
Score:	92.00	Matches:	18
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-302-172-876 (1-583)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         56 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109
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RESULT 14
US-10-211-689-29
; Sequence 29, Application US/10211689
; Publication No. US20030232347A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khramstov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13

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;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(599)
US-10-211-689-29

Alignment Scores:
Pred. No.:              4.75e-06        Length:         684
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-13 (1-18) x US-10-211-689-29 (1-684)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db         18 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 71

RESULT 15
US-10-211-689-41
; Sequence 41, Application US/10211689
; Publication No. US20030232347A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John II
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Khramstov, Nikolai V.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Pena, Carol A.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-416B
;  CURRENT APPLICATION NUMBER: US/10/211,689
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/311751
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/310,802
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/310,795
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/311,292
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/361,159
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: 60/373,050
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: 60/380,970
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/311,979
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 60/381,030
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/323,944
;  PRIOR FILING DATE: 2001-09-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 41
;   LENGTH: 709
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(709)
US-10-211-689-41

Alignment Scores:
Pred. No.:              4.95e-06        Length:         709
Score:                  92.00           Matches:        18
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     7               Gaps:           0

US-09-827-854A-13 (1-18) x US-10-211-689-41 (1-709)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 67


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Job time : 130.918 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 22:11:12 ; Search time 3.12303 Seconds
(without alignments)
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Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTFLAGCQA 18

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss04
-USER=US09827854_@CGN_1_1_39_@runat_14062006_081840_27029 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		75	81.5	5515	6	US-10-524-021-1	Sequence 1, Appli
2		50	54.3	3440	6	US-10-449-902-18081	Sequence 18081, A
3		48	52.2	1503	6	US-10-953-349-22323	Sequence 22323, A
4		48	52.2	118899	7	US-11-189-279-64	Sequence 64, Appl
5		47	51.1	2553	6	US-10-449-902-17095	Sequence 17095, A
6	c	45	48.9	151830	6	US-10-519-335-37	Sequence 37, Appl
7	c	44	47.8	586	6	US-10-449-902-28383	Sequence 28383, A
8		44	47.8	1371	6	US-10-449-902-10702	Sequence 10702, A
9	c	44	47.8	1425	6	US-10-449-902-1107	Sequence 1107, Ap
10		44	47.8	2618	6	US-10-449-902-25053	Sequence 25053, A
11	c	44	47.8	2794	6	US-10-449-902-13084	Sequence 13084, A
12		44	47.8	2892	6	US-10-449-902-27239	Sequence 27239, A
13		43.5	47.3	2260	6	US-10-449-902-21037	Sequence 21037, A
14		43.5	47.3	2265	6	US-10-449-902-15333	Sequence 15333, A
15		43.5	47.3	2392	6	US-10-449-902-24008	Sequence 24008, A
16		43	46.7	957	6	US-10-471-571A-2653	Sequence 2653, Ap
17		43	46.7	1063	6	US-10-449-902-21253	Sequence 21253, A
18	c	43	46.7	1146	7	US-11-217-529-2240	Sequence 2240, Ap
19		43	46.7	2353	6	US-10-449-902-26166	Sequence 26166, A
20		42	45.7	856	6	US-10-449-902-490	Sequence 490, App
21	c	42	45.7	1842	6	US-10-449-902-18852	Sequence 18852, A
22		42	45.7	1954	6	US-10-449-902-27158	Sequence 27158, A
23	c	42	45.7	2187	6	US-10-449-902-21820	Sequence 21820, A
24	c	42	45.7	2249	7	US-11-293-697-442	Sequence 442, App
25	c	42	45.7	2930	7	US-11-145-307A-1	Sequence 1, Appli
26		42	45.7	2934	7	US-11-217-529-79433	Sequence 79433, A
27		42	45.7	3486	6	US-10-449-902-12686	Sequence 12686, A
28		42	45.7	4282	6	US-10-449-902-18815	Sequence 18815, A
29		41.5	45.1	1477	6	US-10-953-349-13080	Sequence 13080, A
30		41.5	45.1	1486	6	US-10-953-349-22075	Sequence 22075, A
31	c	41.5	45.1	1842	6	US-10-449-902-7083	Sequence 7083, Ap
32		41.5	45.1	2484	6	US-10-449-902-14774	Sequence 14774, A
33		41.5	45.1	17402	7	US-11-296-119-8	Sequence 8, Appli
34	c	41	44.6	365	6	US-10-473-173-297	Sequence 297, App
35	c	41	44.6	381	7	US-11-217-529-166913	Sequence 166913,
36	c	41	44.6	489	7	US-11-217-529-80129	Sequence 80129, A
37	c	41	44.6	510	6	US-10-488-619-2087	Sequence 2087, Ap
38		41	44.6	1391	6	US-10-449-902-8455	Sequence 8455, Ap
39	c	41	44.6	1481	6	US-10-449-902-18066	Sequence 18066, A
40		41	44.6	1635	6	US-10-953-349-36046	Sequence 36046, A
41		41	44.6	1654	6	US-10-449-902-20458	Sequence 20458, A
42		41	44.6	2307	7	US-11-293-697-1429	Sequence 1429, Ap
43		41	44.6	2891	6	US-10-449-902-24160	Sequence 24160, A
44		41	44.6	3072	7	US-11-293-697-1127	Sequence 1127, Ap
45		40	43.5	640	6	US-10-449-902-17714	Sequence 17714, A

ALIGNMENTS

RESULT 1
US-10-524-021-1
; Sequence 1, Application US/10524021
; Publication No. US20060099590A1
; GENERAL INFORMATION:
; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
; APPLICANT: YAMADA, Yoshiji
; APPLICANT: YOKOTA, Mitsuhiro
; TITLE OF INVENTION: Method for diagnosing a risk of restenosis after percutaneous c
; TITLE OF INVENTION: intervention
; FILE REFERENCE: C0200501
; CURRENT APPLICATION NUMBER: US/10/524,021
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: JP P2002-233041
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-524-021-1

Alignment Scores:

Pred. No.:	0.00103	Length:	5515
Score:	75.00	Matches:	16
Percent Similarity:	88.9%	Conservative:	0
Best Local Similarity:	88.9%	Mismatches:	2
Query Match:	81.5%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-524-021-1 (1-5515)

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Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db       1871 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGTATGGGGGCG 1924
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RESULT 2
US-10-449-902-18081
; Sequence 18081, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18081
; LENGTH: 3440
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK068492
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18081

Alignment Scores:

Pred. No.:	16.8	Length:	3440
Score:	50.00	Matches:	9
Percent Similarity:	71.4%	Conservative:	1
Best Local Similarity:	64.3%	Mismatches:	4
Query Match:	54.3%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-18081 (1-3440)

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Db        458 GTTCTGTGGGTTGCTTTGTTACTATGTTTTTTGTGTTCATGT 499
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RESULT 3
US-10-953-349-22323
; Sequence 22323, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22323
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22323

Alignment Scores:

Pred. No.:	13.7	Length:	1503
Score:	48.00	Matches:	8
Percent Similarity:	66.7%	Conservative:	4
Best Local Similarity:	44.4%	Mismatches:	6
Query Match:	52.2%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-953-349-22323 (1-1503)

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Db       1051 ATGGGGATATTGTGGGCCCCCCTCTGCCTCACTCACGTTCCCGGTTGCAACTCT 1104
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RESULT 4
US-11-189-279-64
; Sequence 64, Application US/11189279
; Publication No. US20060115829A1
; GENERAL INFORMATION:
; APPLICANT: MAO, LI
; APPLICANT: WANG, JIE
; APPLICANT: LUO, WANG
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: UTXC:875US
; CURRENT APPLICATION NUMBER: US/11/189,279
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: 60/598,554
; PRIOR FILING DATE: 2004-08-03
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 118899
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-189-279-64

Alignment Scores:

Pred. No.:	3.17e+03	Length:	118899
Score:	48.00	Matches:	7
Percent Similarity:	80.0%	Conservative:	5
Best Local Similarity:	46.7%	Mismatches:	3
Query Match:	52.2%	Indels:	0
DB:	7	Gaps:	0

US-09-827-854A-13 (1-18) x US-11-189-279-64 (1-118899)

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Qy          3 ValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGln 17
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Db      57048 CTTCTCTGGTCTCCGATTTCACTGGTGTTTCTCTCTGGCTGCCAG 57092
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RESULT 5
US-10-449-902-17095
; Sequence 17095, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17095
; LENGTH: 2553
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK067558
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-17095

Alignment Scores:

Pred. No.:	39.9	Length:	2553

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Score:                 47.00          Matches:       8
Percent Similarity:    66.7%          Conservative:  4
Best Local Similarity: 44.4%          Mismatches:    6
Query Match:           51.1%          Indels:        0
DB:                    6              Gaps:          0

US-09-827-854A-13 (1-18) x US-10-449-902-17095 (1-2553)

Qy          1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db       1105 ATGTCATTGATATGGATGGGCTTGGTGGTAACATACCTCACCGGTGCAGGTGCT 1158

RESULT 6
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
;  APPLICANT: Cavarec, Laurent
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Destenaves, Benoit
;  APPLICANT:  Gonthier, Catherine
;  APPLICANT:  Elias, Isabelle
;  TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
;  TITLE OF INVENTION:  TREATMENT OF MENTAL DISORDERS
;  FILE REFERENCE: G-194US03PCT
;  CURRENT APPLICATION NUMBER: US/10/519,335
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US 60/391,359
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 151830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (60402)..(60402)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (61110)..(61110)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98207)..(98207)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98208)..(98208)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98209)..(98209)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98210)..(98210)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (98211)..(98211)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (99743)..(99743)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (108055)..(108055)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109094)..(109094)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (109125)..(109125)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (118900)..(118900)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119024)..(119052)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119053)..(119112)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119115)..(119121)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119123)..(119123)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (141674)..(141674)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142063)..(142063)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142137)..(142137)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (142967)..(142967)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143077)..(143077)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143506)..(143506)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143587)..(143587)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143629)..(143629)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (149079)..(149079)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5363)..(5363)
;   OTHER INFORMATION: n = a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8080)..(8080)
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; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10296)..(10296)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14528)..(14528)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15336)..(15336)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15457)..(15457)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16288)..(16288)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16306)..(16307)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16316)..(16316)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16397)..(16397)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56012)..(56012)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57662)..(57662)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(54)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (55)..(124)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (91147)..(91244)
; OTHER INFORMATION: exon 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: (93669)..(93834)
; OTHER INFORMATION: exon 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: (96310)..(96422)
; OTHER INFORMATION: exon 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: (99546)..(99723)
; OTHER INFORMATION: exon 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: (125441)..(125605)

Alignment Scores:

Pred. No.:	1.46e+04	Length:	151830
Score:	45.00	Matches:	9
Percent Similarity:	76.5%	Conservative:	4
Best Local Similarity:	52.9%	Mismatches:	4
Query Match:	48.9%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-519-335-37 (1-151830)

```
Qy          2 LysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ::::::|||   ||||||:::   :::   |||   ||||||||||||||||
Db     151567 AGGTTGTTGGTGGCGGCGATGGCAATGATGTTCTCAGCCGGGTGCCAGGCC 151517
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RESULT 7
US-10-449-902-28383/c
; Sequence 28383, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28383
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK103825
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-28383

Alignment Scores:

Pred. No.:	21.9	Length:	586
Score:	44.00	Matches:	7
Percent Similarity:	71.4%	Conservative:	3
Best Local Similarity:	50.0%	Mismatches:	4
Query Match:	47.8%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-28383 (1-586)

```
Qy          3 ValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCys 16
              |||:::|||            :::|||:::||||||||||||
Db        346 GTCATGTGGACGCCGTCCCAGTTGACGTACTTGGCCGGCTGC 305
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RESULT 8
US-10-449-902-10702
; Sequence 10702, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10702
; LENGTH: 1371

; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK108050
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-10702

Alignment Scores:

Pred. No.:	63.3	Length:	1371
Score:	44.00	Matches:	7
Percent Similarity:	71.4%	Conservative:	3
Best Local Similarity:	50.0%	Mismatches:	4
Query Match:	47.8%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-10702 (1-1371)

```
Qy          3 ValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCys 16
              |||:::|||           :::|||:::|||||||||||
Db        787 GTCATGTGGACGCCGTCCCAGTTGACGTACTTGGCCGGCTGC 828
```

RESULT 9
US-10-449-902-1107/c
; Sequence 1107, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1107
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK059168
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-1107

Alignment Scores:

Pred. No.:	66.4	Length:	1425
Score:	44.00	Matches:	7
Percent Similarity:	71.4%	Conservative:	3
Best Local Similarity:	50.0%	Mismatches:	4
Query Match:	47.8%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-1107 (1-1425)

```
Qy          3 ValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCys 16
              |||:::|||           :::|||:::|||||||||||
Db       1054 GTCATGTGGACGCCGTCCCAGTTGACGTACTTGGCCGGCTGC 1013
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RESULT 10
US-10-449-902-25053
; Sequence 25053, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25053
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK100495
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-25053

Alignment Scores:

Pred. No.:	142	Length:	2618
Score:	44.00	Matches:	8
Percent Similarity:	81.8%	Conservative:	1
Best Local Similarity:	72.7%	Mismatches:	2
Query Match:	47.8%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-25053 (1-2618)

```
Qy          5 TrpAlaAlaLeuLeuValThrPheLeuAlaGly 15
              ||||||||||||||||||||   :::   |||
Db       2056 TGGGCGGCGCTTCTGGTGACCCTAATCGGCGGA 2088
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RESULT 11
US-10-449-902-13084/c
; Sequence 13084, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13084
; LENGTH: 2794
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK110432
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-13084

Alignment Scores:

Pred. No.:	154	Length:	2794
Score:	44.00	Matches:	10
Percent Similarity:	76.5%	Conservative:	3
Best Local Similarity:	58.8%	Mismatches:	4
Query Match:	47.8%	Indels:	0
DB:	6	Gaps:	0

US-09-827-854A-13 (1-18) x US-10-449-902-13084 (1-2794)

```
Qy          2 LysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
              ::::::|||   ||||||||||||   :::   ||||||||||||   |||
Db       1516 CAGCTGCTGCTGGCCGCGCTGCTGCCCTCCAGCCTGGCAGGCTGTCACGCC 1466
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RESULT 12
US-10-449-902-27239
; Sequence 27239, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27239
;   LENGTH: 2892
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK102681
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27239

Alignment Scores:
Pred. No.:              160          Length:        2892
Score:                  44.00        Matches:       7
Percent Similarity:     75.0%        Conservative:  2
Best Local Similarity:  58.3%        Mismatches:    3
Query Match:            47.8%        Indels:        0
DB:                     6            Gaps:          0

US-09-827-854A-13 (1-18) x US-10-449-902-27239 (1-2892)

Qy          5 TrpAlaAlaLeuLeuValThrPheLeuAlaGlyCys 16
              ||||||   :::      |||||||||:::||||||
Db       1532 TGGGCCATGATGTGCCAGACCTTCCTATCGGGATGC 1567

RESULT 13
US-10-449-902-21037
; Sequence 21037, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21037
;   LENGTH: 2260
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK071336
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-21037

Alignment Scores:
Pred. No.:              145          Length:        2260
Score:                  43.50        Matches:       9
Percent Similarity:     73.7%        Conservative:  5
Best Local Similarity:  47.4%        Mismatches:    4
Query Match:            47.3%        Indels:        1
DB:                     6            Gaps:          1

US-09-827-854A-13 (1-18) x US-10-449-902-21037 (1-2260)

Qy          1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
              |||:::   ||||||      :::   |||:::::|||||||:::   |||||||||
Db       1341 ATGGAAAACTTGTGGCAGTTGGTGTAGTTGATATCCTTCCTAAGTGCCTGTCAAGCA 1397

RESULT 14
US-10-449-902-15333
; Sequence 15333, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15333
;   LENGTH: 2265
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK065861
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15333

Alignment Scores:
Pred. No.:              145          Length:        2265
Score:                  43.50        Matches:       9
Percent Similarity:     73.7%        Conservative:  5
Best Local Similarity:  47.4%        Mismatches:    4
Query Match:            47.3%        Indels:        1
DB:                     6            Gaps:          1

US-09-827-854A-13 (1-18) x US-10-449-902-15333 (1-2265)

Qy          1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
              |||:::   ||||||      :::   |||:::::|||||||:::   |||||||||
Db       1401 ATGGAAAACTTGTGGCAGTTGGTGTAGTTGATATCCTTCCTAAGTGCCTGTCAAGCA 1457

RESULT 15
US-10-449-902-24008
; Sequence 24008, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 24008
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1106)..(1106)
; OTHER INFORMATION: "n"=any one base of a, t, c, or g
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK099450
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24008

Alignment Scores:

Pred. No.:	156	Length:	2392
Score:	43.50	Matches:	9
Percent Similarity:	73.7%	Conservative:	5
Best Local Similarity:	47.4%	Mismatches:	4
Query Match:	47.3%	Indels:	1
DB:	6	Gaps:	1

US-09-827-854A-13 (1-18) x US-10-449-902-24008 (1-2392)

```
Qy          1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
              |||:::   ||||||      :::   |||::::::||||||:::   |||||||||
Db       1369 ATGGAAAACTTGTGGCAGTTGGTGTAGTTGATATCCTTCCTAAGTGCCTGTCAAGCA 1425
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Search completed: June 14, 2006, 22:15:10
Job time : 9.12303 secs